

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 04:12:36 ; Search time 74 Seconds
(without alignments)
1829.272 Million cell updates/sec

Title: US-09-721-341-2
1819
Perfect score: 1 MALEQNQSTDYDENEMNG.....VEPPFDSGPTPTSTFSI 350
Sequence:

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues
Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

1: geneeqp1980s:*
2: geneeqp1990s:*
3: geneeqp2000s:*
4: geneeqp2001s:*
5: geneeqp2002s:*
6: geneeqp2003as:*
7: geneeqp2003bs:*
8: geneeqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	2	AAW93169 Human HFI
2	1819	100.0	350	2	AAW93169 Human HFI
3	1819	100.0	350	2	AAW93169 Human HFI
4	1819	100.0	350	2	AAW93169 Human HFI
5	1819	100.0	350	2	AAW93169 Human HFI
6	1819	100.0	350	2	AAW93169 Human HFI
7	1819	100.0	350	2	AAW93169 Human HFI
8	1819	100.0	350	2	AAW93169 Human HFI
9	1819	100.0	350	2	AAW93169 Human HFI
10	1819	100.0	350	2	AAW93169 Human HFI
11	1819	100.0	350	2	AAW93169 Human HFI
12	1819	100.0	350	2	AAW93169 Human HFI
13	1819	100.0	350	2	AAW93169 Human HFI
14	1819	100.0	350	2	AAW93169 Human HFI
15	1819	100.0	350	2	AAW93169 Human HFI
16	1819	100.0	350	2	AAW93169 Human HFI
17	1819	100.0	350	2	AAW93169 Human HFI
18	1819	100.0	350	2	AAW93169 Human HFI
19	1819	100.0	350	2	AAW93169 Human HFI
20	1819	100.0	350	2	AAW93169 Human HFI
21	1819	100.0	350	2	AAW93169 Human HFI
22	1819	100.0	350	2	AAW93169 Human HFI
23	1819	100.0	350	2	AAW93169 Human HFI
24	1819	100.0	350	2	AAW93169 Human HFI
25	1819	100.0	350	2	AAW93169 Human HFI

26	1810	99.5	350	8	ADQ75082 Human G P
27	1808	99.4	350	3	AA837788 Human TSC
28	1804	99.2	350	8	ADG65525 Human end
29	1803	99.1	350	7	ADP60885 Human GPC
30	1728	95.0	333	2	AA57289 Human BGC
31	1620	89.1	350	4	AA67238 Human ac1
32	1620	89.1	350	7	ADA10817 Cow B1gna
33	1593	87.6	350	8	ADO29238 Mouse GPC
34	1591	87.5	350	2	AA57291 Mouse BGC
35	1275	70.1	246	2	AA57292 Human BGC
36	1257	69.1	242	4	AAW9949 Human exp
37	1212	66.6	263	2	AA30126 A seven-P
38	862	47.4	164	4	AB11162 Human ORP
39	862	47.4	164	4	AAW9310 Human pro
40	824	45.3	159	3	AA841786 Human ORF
41	761	41.8	175	4	AAU18115 Novel hum
42	761	41.8	175	4	AAU18669 Renal and
43	761	41.8	175	4	AAU21655 Novel hum
44	761	41.8	175	4	AAW9976 Human exp
45	761	41.8	175	4	AB10276 Human CDN

ALIGNMENTS

RESULT 1	AAW93169	standard; protein; 350 AA.
ID	AAW93169	standard; protein; 350 AA.
XX	AAW93169;	
AC	AAW93169;	
DT	24-MAY-1999	(first entry)
XX	Human HPIA01 protein.	
DE	Human HPIA01 protein.	
XX		
XX	HPIA01; G-coupled receptor; disease susceptibility; diagnosis; immunise;	
KW	treatment; FIAO1 protein; gene therapy; immune response; vaccine; HIV-2;	
KW	inoculate; bacterial; fungal; protozoan; viral; infection; HIV-1; cancer;	
KW	diabetes; anorexia; bulimia; Parkinson's disease; acute heart failure;	
KW	hypotension; hypertension; urinary retention; osteoporosis; allergy;	
KW	angina pectoris; myocardial infarction; ulcer; asthma; schizophrenia;	
KW	benign prostatic hyperplasia; psychotic disorder; neurological disorder;	
KW	anxiety; manic depression; delirium; dementia; severe mental retardation;	
KW	dyskinesia; Huntington's disease; Gilles de la Tourette's syndrome;	
KW	linkage analysis; gene mapping; human.	
XX		
OS	Homo sapiens.	
XX		
PN	EP899333-A2.	
PD	03-MAR-1999.	
XX		
PF	17-FEB-1998;	98EP-00301170.
XX		
PR	15-AUG-1997;	97US-0055895P.
XX		
PR	27-OCT-1997;	97US-00962922.
XX		
PA	(SMK) SMITHKLINE BEECHAM CORP.	
PI	Billie CE;	
XX		
DR	WPI: 1999-144803/13.	
XX		
DR	N-P5DB; AA22557.	
PT	New G-coupled receptor (HPIA01) polypeptide and polynucleotide - useful	
PT	as diagnostic reagents and for prevention and treatment of cancer, HIV	
PT	infections and Parkinson's disease.	
XX		
PS	Claim 1; Page 22-23; 27pp; English.	
XX		
CC	This sequence represents a G-coupled receptor, HPIA01 which is useful	
CC	for diagnosing susceptibility to diseases by detecting mutations in the	
CC	HPIA01 gene, and can diagnose diseases associated with HPIA01 protein	

CC imbalance by determining HFI041 polypeptide expression levels. Agonists
 CC and antagonists of the protein can be used in treatment to activate
 CC (agonist) or inhibit (antagonist) HFI041 activity, in addition to direct
 CC administration of antisense sequences to prevent expression, or HFI041
 CC polynucleotides to treat conditions associated with a lack of HFI041
 CC protein. Gene therapy may also be used to affect endogenous HFI041
 CC polypeptide expression. HFI041 antibodies are useful for inducing an
 CC immune response to immune and prevent disease, and for isolating
 CC HFI041 clones or purifying the polypeptides by affinity chromatography.
 CC HFI041 polypeptides can be administered directly or as a vaccine to
 CC inoculate against disease. Diseases diagnosed, prevented and treated
 CC include bacterial, fungal, protozoan and viral infections, particularly
 CC HIV-1 or -2 infections; cancer; diabetes; anorexia; bulimia; Parkinson's
 CC disease; acute heart failure; hypotension; hypertension; urinary
 CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
 CC asthma; allergies; benign prostatic hypertrophy; and psychotic and
 CC neurological disorders, including anxiety, schizophrenia, manic
 CC depression, delirium, dementia, severe mental retardation and dyskinesias
 CC such as Huntington's disease or Gilles de la Tourette's syndrome. The
 CC HFI041 polypeptide is also useful for mapping the gene to a chromosome,
 CC allowing gene inheritance to be studied through linkage analysis
 XX

Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALLEONOSTDYEEENKNGTGYDYSQYELICIKEDVREPAKVFLLPFLTIVFVIGLAGNS 60
 DB 1 MALLEONOSTDYEEENKNGTGYDYSQYELICIKEDVREPAKVFLLPFLTIVFVIGLAGNS 60
 QY 61 MVVAIYAAYKKORTKTIDVYIILNLAADVLLFLTPFMVANAHAHVGLGKIMCKITSAIYT 120
 DB 61 MVVAIYAAYKKORTKTIDVYIILNLAADVLLFLTPFMVANAHAHVGLGKIMCKITSAIYT 120
 QY 121 LNFVSGMOFLACISIDRYVAATKVPQSQGVGKPCWIIICCVMAAAILLSIPOLVFTYVND 180
 DB 121 LNFVSGMOFLACISIDRYVAATKVPQSQGVGKPCWIIICCVMAAAILLSIPOLVFTYVND 180
 QY 181 NARCTPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNKRISPLK 240
 DB 181 NARCTPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNKRISPLK 240
 QY 241 VLLTVIVIVITQLPNIVKFCRAIDIIYSLITSCKMSKRMIDAIQVTSIALFHSCLNP 300
 DB 241 VLLTVIVIVITQLPNIVKFCRAIDIIYSLITSCKMSKRMIDAIQVTSIALFHSCLNP 300
 QY 301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVBEFPDSEGPTEPTSTFSI 350
 DB 301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVBEFPDSEGPTEPTSTFSI 350

RESULT 2
 AAY17435
 ID AAY17435 standard; protein; 350 AA.

AC AAY17435;

DT 29-JUL-1999 (first entry)

DE Human signal peptide-containing protein SP-16.

KW Human; signal peptide-containing protein; SP; cell proliferation; cancer;
 KM neuronal disorder; immune response; detection.

OS Homo sapiens.
 XX
 XX WO924463-A2.
 PN
 XX
 PD 20-MAY-1999.
 XX
 PF 04-NOV-1998; 98WO-US023578.

XX 07-NOV-1997; 97US-00966316.
 PR
 XX
 PA (INCY-) INCYTE PHARM INC.

PI Lal P, Au-Young J, Reddy R, Murry LE, Machur P;

XX WPI; 1999-337694/28.

DR N-PSDB; AAX61288.

PT cDNA clones encoding signal peptide-containing proteins.

PS Claim 1; Fig 1; 83pp; English.

XX
 CC The present sequence represents a human signal peptide-containing protein
 CC (SP), designated SP-16. SP proteins can be used to stimulate cell
 CC proliferation or to treat or prevent cancer. SP antagonists are also used
 CC to treat or prevent cancer, and also for treating or preventing neuronal
 CC disorders or immune responses. Polynucleotide sequences complementary to
 CC the SP-encoding polynucleotides are useful for the detection of SP-
 CC encoding nucleic acid molecules in biological samples
 XX

Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALLEONOSTDYEEENKNGTGYDYSQYELICIKEDVREPAKVFLLPFLTIVFVIGLAGNS 60
 DB 1 MALLEONOSTDYEEENKNGTGYDYSQYELICIKEDVREPAKVFLLPFLTIVFVIGLAGNS 60
 QY 61 MVVAIYAAYKKORTKTIDVYIILNLAADVLLFLTPFMVANAHAHVGLGKIMCKITSAIYT 120
 DB 61 MVVAIYAAYKKORTKTIDVYIILNLAADVLLFLTPFMVANAHAHVGLGKIMCKITSAIYT 120
 QY 121 LNFVSGMOFLACISIDRYVAATKVPQSQGVGKPCWIIICCVMAAAILLSIPOLVFTYVND 180
 DB 121 LNFVSGMOFLACISIDRYVAATKVPQSQGVGKPCWIIICCVMAAAILLSIPOLVFTYVND 180
 QY 181 NARCTPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNKRISPLK 240
 DB 181 NARCTPIPRRYIGTSMKALIQMLEICIGFVVPFLMGVCYFTTARTLMKMPNKRISPLK 240
 QY 241 VLLTVIVIVITQLPNIVKFCRAIDIIYSLITSCKMSKRMIDAIQVTSIALFHSCLNP 300
 DB 241 VLLTVIVIVITQLPNIVKFCRAIDIIYSLITSCKMSKRMIDAIQVTSIALFHSCLNP 300
 QY 301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVBEFPDSEGPTEPTSTFSI 350
 DB 301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVBEFPDSEGPTEPTSTFSI 350

RESULT 3
 AAY57290
 ID AAY57290 standard; protein; 350 AA.

AC AAY57290;

DT 05-JUN-2000 (first entry)

DE Human BGCKr protein.

KW BGCKr protein; G-protein coupled receptor; human; chemokine; exocytosis;
 KM cell proliferation; anti-inflammatory; anti-angiogenic; antitumor; HIV;
 KW anti-allergic; antiviral.

OS Homo sapiens.
 XX
 XX WO952945-A2.
 PN
 XX
 PD 21-OCT-1999.
 XX

PF 16-APR-1999; 99WO-US008395.
 XX
 PR 16-APR-1998; 98US-00061753.
 PR 16-APR-1999; 99US-00061753.
 XX
 PA (MILL-) MILLENITUM PHARM INC.
 XX
 PI Gonzalo JA, Gutierrez-Ramos JC;
 XX
 DR WPI, 1999-620375/53.
 DR N-PSDB; AA290528.
 PT New nucleic acid encoding human BGCKr receptor, used e.g. for modulating
 PT inflammation and tumor growth.
 XX
 PS Claim 8; Fig 2A-B; 123pp; English.
 XX
 CC The invention relates to a human BGCKr protein, a G-protein coupled
 CC receptor. The BGCKr protein can be expressed by standard recombinant
 CC methodology. BGCKr are receptor proteins possibly involved in modulation
 CC of proinflammatory or stimulatory functions of chemokines, cell
 CC proliferation, migration, adhesion and targeting, and exocytosis. The
 CC BGCKr nucleic acids and derived proteins (or their variants), antibodies
 CC and modulators are potentially useful for modulating inflammation;
 CC chemottractant activity of leucocytes; angiogenesis; cell proliferation;
 CC tumour growth; allergic reactions and entry of human immune deficiency
 CC virus into cells, for therapeutic or prophylactic purposes. They are also
 CC used for diagnosis and in drug-screening assays. The present sequence
 CC represents the full-length human BGCKr protein
 XX
 SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 2; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.1e-194; Indels 0; Gaps 0;
 Matches 350; Conservative 0; Mismatches 0;

QY 1 MALEQNSTDYEEENMGTYDYSOYELICIKEDVREPAKVPFLPFLTIVPIGGLAGNS 60
 DB 1 MALEQNSTDYEEENMGTYDYSOYELICIKEDVREPAKVPFLPFLTIVPIGGLAGNS 60
 DB 61 MVAIAIYAYKKORTKTDVYILNLAVADLLFLTPFMAVAVAHGWLGIKIMCKITSALYT 120
 DB 61 MVAIAIYAYKKORTKTDVYILNLAVADLLFLTPFMAVAVAHGWLGIKIMCKITSALYT 120
 QY 121 LNFVSGMOLACISIRYVAVTVKPSQSGVGRKCMWICFCVMAAIIILSTPOLVFYTVND 180
 DB 121 LNFVSGMOLACISIRYVAVTVKPSQSGVGRKCMWICFCVMAAIIILSTPOLVFYTVND 180
 QY 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFIRARTLMKPNIKISRPK 240
 DB 181 NARCIPFPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFIRARTLMKPNIKISRPK 240
 QY 241 VLLTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMCKMDIAIQVTESIALFHSGLNP 300
 DB 241 VLLTVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMCKMDIAIQVTESIALFHSGLNP 300
 QY 301 ILVVFSGAFKYNVMYAKKYGSROROSVEEFPDSEPTPTSTFSI 350
 DB 301 ILVVFSGAFKYNVMYAKKYGSROROSVEEFPDSEPTPTSTFSI 350

RESULT 4
 AA94325
 ID AA94325 standard; protein; 350 AA.
 XX
 AC AA94325;
 XX
 DT 11-AUG-2000 (first entry)
 XX
 DE Human seven transmembrane receptor VSHK-1.
 XX
 KW Human; seven transmembrane receptor; VSHK-1; signal transduction.
 XX

OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 6..8
 FT /note= "potential N-glycosylation site"
 FT Modified-site 19..21
 FT /note= "potential N-glycosylation site"
 FT Domain 42..66
 FT /label= Transmembrane_domain
 FT Domain 79..100
 FT /label= Transmembrane_domain
 FT Domain 114..135
 FT /label= Transmembrane_domain
 FT Domain 156..175
 FT /label= Transmembrane_domain
 FT Domain 199..221
 FT /label= Transmembrane_domain
 FT Domain 241..262
 FT /label= Transmembrane_domain
 FT Modified-site 276..278
 FT /note= "potential N-glycosylation site"
 FT Domain 287..308
 FT /label= Transmembrane_domain
 PD WO200026369-A1.
 PD 11-MAY-2000.
 PP 03-NOV-1999; 99WO-US025848.
 PP 04-NOV-1998; 98US-0107112P.
 PR 06-JAN-1999; 99US-0114856P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Khoja H, Shymala V;
 XX
 DR WPI; 2000-365618/31.
 DR N-PSDB; AA94325.
 PT Novel polypeptide comprising a new seven-transmembrane receptor protein
 PT and its encoding polynucleotide, useful for the analysis of VSHK-1.
 XX
 PS Claim 3; Fig 1; 79pp; English.
 XX
 CC The present sequence is VSHK-1, a new seven transmembrane receptor which
 CC contains seven membrane-spanning helical domains that are linked by three
 CC intracellular and three extracellular loops. The gene sequence encoding
 CC VSHK-1 was isolated from a cDNA library. In heart tissue, where VSHK-1 is
 CC predominantly found, three RNA species were identified: a 1.3kb, a 2.0kb,
 CC and a 5.0kb species. The polynucleotide encoding the present sequence
 CC corresponds to the 2.0kb form. The 1.3kb form may result from the use of
 CC an alternative polyadenylation site while transcription of a 3.0kb intron
 CC at nucleotide 74 could account for the 5.0kb species. VSHK-1
 CC polynucleotides can be used as hybridisation probes to detect and measure
 CC VSHK-1 mRNA. They may also be used to identify substances that modulate
 CC the level of VSHK-1 mRNA. The VSHK-1 coding sequence can be integrated
 CC into an expression vector for production of VSHK-1 receptor polypeptides
 CC in host cells. The polypeptides can be used to identify agents which
 CC modulate VSHK-1 receptor signal transduction activity
 XX
 SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 3; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.1e-194; Indels 0; Gaps 0;
 Matches 350; Conservative 0; Mismatches 0;

QY 1 MALEQNSTDYEEENMGTYDYSOYELICIKEDVREPAKVPFLPFLTIVPIGGLAGNS 60
 DB 1 MALEQNSTDYEEENMGTYDYSOYELICIKEDVREPAKVPFLPFLTIVPIGGLAGNS 60
 QY 61 MVAIAIYAYKKORTKTDVYILNLAVADLLFLTPFMAVAVAHGWLGIKIMCKITSALYT 120
 |||

Db 61 MVAIYAAYKKORTKTDVYIILMLAVADLLLLFTLPFWANAVAGWLGKIMCKITSALYT 120

Qy 121 LNFVSGMOFLACISIDRYAAVTKVPSQSGVKPCWIIICCVMAAILLSIPOLVFYTVND 180

Db 121 LNFVSGMOFLACISIDRYAAVTKVPSQSGVKPCWIIICCVMAAILLSIPOLVFYTVND 180

Qy 181 NARCIPIPRRYLGTSMKALIQMLEICIGFVVPFLINGVCYFITARLTMKMPNIIKISRPLK 240

Db 181 NARCIPIPRRYLGTSMKALIQMLEICIGFVVPFLINGVCYFITARLTMKMPNIIKISRPLK 240

Qy 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKRMDDAIQVTSIALFHSCINP 300

Db 241 VLLTVVIVFIVTQLPYNIVKFCRAIDIIYSLITSCMSKRMDDAIQVTSIALFHSCINP 300

Qy 301 ILVFMGASFKYVMKVAKKYGSWROROSVEEFPDSEGPTEPTSTFST 350

Db 301 ILVFMGASFKYVMKVAKKYGSWROROSVEEFPDSEGPTEPTSTFST 350

RESULT 5

AAU08994 standard; protein; 350 AA.

AAU08994;

18-DEC-2001 (first entry)

Human G protein-coupled receptor, GPCR, 2398.

Human; GPCR; G protein-coupled receptor; 2398; cardiac; antiatherosclerotic; analgesic; cyostatic; antianginal; cardiovascular disorder; angiogenesis-related disorder; neural disorder; pain response disorder; inflammatory disorder; atherosclerosis; angina pectoris; myocardial infarction; ischemic heart disease; sudden cardiac death; obesity; hypertensive heart disease; diabetes; prostate cancer-related pain.

Homo sapiens.

Location/Qualifiers

125..141

/label=G_protein_receptor_signature

WO200164882-A2.

07-SEP-2001.

28-FEB-2001; 2001WO-US006543.

29-FEB-2000; 2000US-0186059P.

(MILL-) MILLENNIUM PHARM INC.

Glucksman MA, Galvin KM, Silos-Santiago I;

WPI; 2001-589866/66.

N-PSDB; AAS14572.

Novel G protein coupled receptors and nucleic acids encoding them, for identifying agents for the treatment of cardiac disorders.

Claim 9; Fig 9; 209pp; English.

The invention relates to novel human G protein-coupled receptors (GPCR) named 1983, 52881, 2398, 45449, 50289 and 52872. The novel GPCRs and nucleic acids encoding them are useful for identifying agents for the treatment of cardiovascular disorders, angiogenesis-related disorders, neural disorders, pain response disorders and inflammatory disorders, e.g. atherosclerosis, angina pectoris and myocardial infarction, ischemic heart disease, sudden cardiac death, hypertensive heart disease, diabetes, prostate cancer-related pain, diabetes and obesity. The present sequence represents GPCR 2398

SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 4; Length 350;

Best Local Similarity 100.0%; Pred. No. 1..1e-194; Mismatches 0; Gaps 0;

Matches 350; Conservative 0; Indels 0; Gaps 0;

Qy 1 MLEQNSDYYEENENGTVDYSGYELICIKEDVREPAKFLPVFLTIVFVIGLAGNS 60

RESULT 6

AAAG80119 standard; protein; 350 AA.

AAAG80119;

17-JAN-2002 (first entry)

Human CCR11 protein.

Chemokine; tumour diagnosis; colorectal; prostatic; organ rejection; inflammation; autoimmune disease; metastasis; bronchial asthma; lupus; chronic bowel inflammation; rheumatoid arthritis; cytostatic; antiinflammatory; antineoplastic; immunosuppressive; dermatological; antirheumatic; antiarthritic.

Homo sapiens.

WO200172830-A2.

04-OCT-2001.

02-APR-2001; 2001WO-EP003708.

31-MAR-2000; 2000DE-01016013.

(IPFP-) IPF PHARM GMBH.

(FORS/) FORSMANN U.

Forsmann W, Adermann K, Heitland A, Spodeberg N;

WPI; 2001-626256/72.

Diagnostic agent containing two or more receptor-specific ligands, useful for detecting tumors, inflammation etc., also therapeutic use of ligand inhibitors.

Disclosure; Page 11; 26pp; German.

This invention describes a novel diagnostic agent (A) comprising at least two different ligands (I) for receptors (II) that are implicated in disease. (A) are used for the diagnosis of tumors (especially colorectal

CC or prostatic), organ rejection, inflammation and autoimmune diseases.
 CC Also inhibitors of (1) are used therapeutically against tumors (and their
 CC metastases), inflammation (particularly bronchial asthma or chronic bowel
 CC inflammation), or autoimmune diseases (rheumatoid arthritis or lupus),
 CC where the (cardio)vascular, lymphatic, respiratory, nervous, digestive,
 CC endocrine, motor or urogenital systems or skin are affected, and bone
 CC marrow diseases. The products of the invention are chemokine derivatives
 CC which have cytostatic, antiinflammatory, antitumor, antiproliferative,
 CC immunosuppressive, dermatological, antipneumatic, antiarthritic,
 CC chemokines act on specific tumor and inflammatory cells through a
 CC constellation of chemokine receptors (CR), which control migration and
 CC proliferation of these cells. AAG80045-AAG80128 represent human chemokine
 CC fragments used to illustrate the method of the invention

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 4; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQNSTDYVEENENGTGYDQYELICKEVDREPAKFLVPLTIVVIGLAGNS 60
 DB 1 MLEQNSTDYVEENENGTGYDQYELICKEVDREPAKFLVPLTIVVIGLAGNS 60
 QY 61 MVVAIYAYKKORTKTDVYIILNLAVALDLLFTLPFMAVNAVHGVLAGKIMCKITSALT 120
 DB 61 MVVAIYAYKKORTKTDVYIILNLAVALDLLFTLPFMAVNAVHGVLAGKIMCKITSALT 120
 QY 121 INFVSGMOFLACISIDRYVAATKVPSSQSGVGRPCWIIICFCVMAAILISIPOLVFTYVND 180
 DB 121 INFVSGMOFLACISIDRYVAATKVPSSQSGVGRPCWIIICFCVMAAILISIPOLVFTYVND 180
 QY 181 NARCIPIPRRYGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLMKMPNIXSRPK 240
 DB 181 NARCIPIPRRYGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLMKMPNIXSRPK 240
 QY 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDAIQVETESIALFHSCLNP 300
 DB 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDAIQVETESIALFHSCLNP 300

QY 301 ILYVMSGAFKQYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTSI 350
 DB 301 ILYVMSGAFKQYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTSI 350

RESULT 7
 AAG67237
 ID AAG67237 standard; protein; 350 AA.

XX AC AAG67237;

XX DT 13-NOV-2001 (first entry)

XX DE Amino acid sequence of human chemokine receptor CCR11.

XX KW Human; chemokine receptor; CCR11; G protein coupled receptor;
 KW inflammatory disease; rheumatoid arthritis; inflammatory bowel disease;
 KW asthma; angiodenesis; atherosclerosis vascular association disease;
 KW hypertension; angina pectoris; cardiac arrhythmia; Raynaud's phenomenon;
 KW left ventricular diastolic dysfunction; migraine; preterm labour;
 KW oesophageal spasm; ischaemic stroke; subarachnoid haemorrhage;
 KW myocardial infarction; congestive heart failure; endometriosis;
 KW vasospasm; retinopathy; nephropathy; pulmonary vascular disease.

XX OS Homo sapiens.

XX PN WO200166598-A2.

XX PD 13-SEP-2001.

XX PF 05-MAR-2001; 2001WO-US007073.

XX PR 03-MAR-2000; 2000US-0186928P.

PR 03-MAR-2000; 2000US-0187231P.

XX PA (ICOS-) ICOS CORP.
 XX PI Gray PW, Schweickart VL, Epp A, Raport CJ, Chantry D, Steiner B;
 XX WPI; 2001-541918/60.
 DR N-PSDB; AAH77711.
 PT An isolated polynucleotide encoding the chemokine receptor CCR11, useful
 PT for treating rheumatoid arthritis, inflammatory bowel disease, asthma,
 PT angiodenesis, atherosclerosis, cardiac arrhythmias, Raynaud's phenomenon
 PT and migraine.

XX PS Claim 13; Page 96-97; 110pp; English.

XX CC The present sequence represents the human chemokine receptor CCR11. CCR11
 CC is a member of the G protein coupled receptor family. A CCR11
 CC polypeptide, its inhibitor, an antibody, or other modulator of CCR11
 CC expression or biological activity, is useful for treating many
 CC inflammatory diseases, for example, rheumatoid arthritis, inflammatory
 CC bowel disease, and asthma. They are also useful for treating
 CC angiodenesis, atherosclerosis vascular association diseases which may
 CC include but are not limited to hypertension, angina pectoris, cardiac
 CC arrhythmias, left ventricular diastolic dysfunction, Raynaud's
 CC phenomenon, migraine, preterm labour, oesophageal spasm, ischaemic
 CC stroke, subarachnoid haemorrhage, myocardial infarction, congestive heart
 CC failure, endometriosis, vasospasm, retinopathy, nephropathy, or pulmonary
 CC vascular disease

XX SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 4; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQNSTDYVEENENGTGYDQYELICKEVDREPAKFLVPLTIVVIGLAGNS 60
 DB 1 MLEQNSTDYVEENENGTGYDQYELICKEVDREPAKFLVPLTIVVIGLAGNS 60

QY 61 MVVAIYAYKKORTKTDVYIILNLAVALDLLFTLPFMAVNAVHGVLAGKIMCKITSALT 120
 DB 61 MVVAIYAYKKORTKTDVYIILNLAVALDLLFTLPFMAVNAVHGVLAGKIMCKITSALT 120

QY 121 INFVSGMOFLACISIDRYVAATKVPSSQSGVGRPCWIIICFCVMAAILISIPOLVFTYVND 180
 DB 121 INFVSGMOFLACISIDRYVAATKVPSSQSGVGRPCWIIICFCVMAAILISIPOLVFTYVND 180

QY 181 NARCIPIPRRYGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLMKMPNIXSRPK 240
 DB 181 NARCIPIPRRYGTSMKALIQMLEICIGFVVPFLIMGVCYFTARTLMKMPNIXSRPK 240

QY 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDAIQVETESIALFHSCLNP 300
 DB 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDAIQVETESIALFHSCLNP 300

QY 301 ILYVMSGAFKQYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTSI 350
 DB 301 ILYVMSGAFKQYVMKAKKYGSMRQROSVSEFPDSEGPTEPTSTSI 350

RESULT 8
 AAE37348
 ID AAE37348 standard; protein; 350 AA.

XX AC AAE37348;

XX DT 27-AUG-2003 (first entry)

XX DE Human C-C chemokine receptor type 11 (CC CKR-11), 2398 protein.

XX KW Human; cardiovascular disorder; coronary artery disease; bradycardia;
 KW stenosis; cardiac hypertrophy; ischaemia reperfusion injury; angina;

KM arteriosclerosis; coronary artery ligation; rheumatic heart disease;
 KM heart failure; hypertension; cardiomyopathy; myocardial infarction;
 KM arterial inflammation; microembolism; atherosclerosis; endocarditis;
 KM vascular heart disease; valvular disease; arrhythmia; gene therapy;
 KM sinus node dysfunction; C-C chemokine receptor type 11; CC CR-11;
 KM receptor.
 KM Homo sapiens.
 OS
 XX
 XX MO2003039341-A2.
 PN
 XX
 PD 15-MAY-2003.
 PF
 XX 05-NOV-2002; 2002WO-US035538.
 XX
 XX 05-NOV-2001; 2001US-0339582P.
 PR
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX Logan TJ, Chun M, Galvin KM;
 PI
 XX
 XX WPI: 2003-441437/41.
 DR
 XX N-PSDB; AAD56515.
 DR
 XX
 XX Treating a subject having a cardiovascular disorder, e.g. angina,
 PT arrhythmia, or restenosis, comprises administering a 139, 258, 1261,
 PT 1486, 2398, 2414, 7660, 8587, 10183, 10550, 12680, 17921, 32248 or
 PT 93804 modulator.
 PS
 XX Disclosure; Page 105-106; 124pp; English.
 XX
 XX The invention relates to methods and compositions for treating a subject
 CC having a cardiovascular disorder using 139, 258, 1261, 1486, 2398, 2414,
 CC 7660, 8587, 10183, 10550, 12680, 17921, 32248, 60489 or 93804 modulator.
 CC The invention is useful for treating a cardiovascular disorder, including
 CC arteriosclerosis, atherosclerosis, vascular wall remodeling, restenosis,
 CC cardiac hypertrophy, ischemia reperfusion injury, arterial inflammation,
 CC ventricular remodeling, rapid ventricular pacing, tachycardia, coronary
 CC microembolism, bradycardia, pressure overload, aortic bending, coronary
 CC artery ligation, vascular heart disease, valvular disease, including but
 CC not limited to, valvular degeneration caused by calcification, rheumatic
 CC heart disease, endocarditis, or complications of artificial valves;
 CC atrial fibrillation, long-QT syndrome, congestive heart failure, sinus
 CC node dysfunction, angina, heart failure, hypertension, atrial flutter,
 CC atrial fibrillation, pericardial disease, including but not limited to
 CC pericardial effusion and pericarditis, cardiomyopathies (e.g. dilated
 CC cardiomyopathy or idiopathic cardiomyopathy), myocardial infarction,
 CC coronary artery disease, coronary artery spasm, ischemic disease,
 CC arrhythmia, sudden cardiac death, and cardiovascular developmental
 CC disorders. The invention is also useful in gene therapy. The present
 CC sequence is human C-C chemokine receptor type 11 (CC CR-11) protein.
 CC This sequence is used to illustrate the method of the invention
 XX
 XX Sequence 350 AA;
 SQ

Query Match 100.0%; Score 1819; DB 6; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1,1e-194;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALLEONQSTDDYYEENENNGTDDYSEYELICIKEDYREPAKFLPLPLTLTVYTGAGNS 60
 DB 1 MALLEONQSTDDYYEENENNGTDDYSEYELICIKEDYREPAKFLPLPLTLTVYTGAGNS 60
 QY 61 MVAATYAYYKKORTKTDVYILNLAVALDLLLFTLPPMAVNAHGWVLGKIMCKTISALYT 120
 DB 61 MVAATYAYYKKORTKTDVYILNLAVALDLLLFTLPPMAVNAHGWVLGKIMCKTISALYT 120
 QY 121 LNFVSGMQLACISIDRYAVAVTKVPSQSGVGRWCWIIICFCVMAAAILISIPOLVFYTVND 180
 DB 121 LNFVSGMQLACISIDRYAVAVTKVPSQSGVGRWCWIIICFCVMAAAILISIPOLVFYTVND 180
 QY 181 NARCPIDIPRYIGTSKALIQMLEICIGRVVPLIMGVCYFTARTLMKMPNIXISRPXK 240
 DB 181 NARCPIDIPRYIGTSKALIQMLEICIGRVVPLIMGVCYFTARTLMKMPNIXISRPXK 240

DB 181 NARCPIDIPRYIGTSKALIQMLEICIGRVVPLIMGVCYFTARTLMKMPNIXISRPXK 240
 QY 241 VLLTVYVFIYVTLQPLPYNIVKFCRAIDIIYSLTSCNMSKRMIDIAQVETESIALFHSCLNP 300
 DB 241 VLLTVYVFIYVTLQPLPYNIVKFCRAIDIIYSLTSCNMSKRMIDIAQVETESIALFHSCLNP 300
 QY 301 ILVFMGASFKNYVMKVAKKTGSWRRQSQSVEEPPDSGPEPTSTSI 350
 DB 301 ILVFMGASFKNYVMKVAKKTGSWRRQSQSVEEPPDSGPEPTSTSI 350
 RESULT 9
 ABP81716
 ID ABP81716 standard; protein; 350 AA.
 XX
 XX ABP81716;
 AC
 XX 04-MAR-2003 (first entry)
 DT
 XX Human C-C chemokine receptor 11 protein SEQ ID NO:607.
 DE
 XX
 XX G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
 KM G protein-coupled receptor modulator; antibody; immune-related disease;
 KM growth-related disease; cell regeneration-related disease; AIDS; cancer;
 KM immunological-related cell proliferative disease; autoimmune disease;
 KM Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
 KM osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
 KM graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
 KM psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
 KM mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
 KM hypertension; hypotension; renal disorder; Rheumatoid arthritis; trauma;
 KM ulcer.
 KM Homo sapiens.
 OS
 XX
 XX MO200261087-A2.
 PN
 XX
 XX 08-AUG-2002.
 PD
 XX
 XX 19-DEC-2001; 2001WO-US050107.
 PF
 XX
 XX 19-DEC-2000; 2000US-0257144P.
 PR
 XX (LIFE-) LIFESPAN BIOSCIENCES INC.
 PA
 XX Burner GC, Roush CL, Brown JB;
 PI
 XX WPI: 2003-046718/04.
 DR
 XX N-PSDB; AB242562.
 DR
 XX
 XX New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 PS
 XX Disclosure; Fig 1; 523pp; English.
 XX
 XX The present invention describes antigenic peptides (I) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related disease, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute

CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, peristalsis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. AB242523 to AB242869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention

XX Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 6; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQNSTDYEEENENGTVDYSQYELICKEDEVEPAKFLPVFLTIVFVIGLAGNS 60
 DB 1 MLEQNSTDYEEENENGTVDYSQYELICKEDEVEPAKFLPVFLTIVFVIGLAGNS 60
 QY 61 MVAIAYAYKKORTKTDVYILNLAVALDLLFTLPMAVNAVHGWLGKIMCKITSAALT 120
 DB 61 MVAIAYAYKKORTKTDVYILNLAVALDLLFTLPMAVNAVHGWLGKIMCKITSAALT 120
 QY 121 LNFVSGMOPACISIDRYAVAVTKVPSQSGVGKPCWIIICPCVMAAILLSIPOLVFYTVND 180
 DB 121 LNFVSGMOPACISIDRYAVAVTKVPSQSGVGKPCWIIICPCVMAAILLSIPOLVFYTVND 180
 QY 181 NARCIPIPPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIXISRPXK 240
 DB 181 NARCIPIPPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIXISRPXK 240
 QY 241 VLLTVIVIVITVQLPNIYKFCRAIDIIYSLTSCMSKRMIDAIQVETSIALFHSCLNP 300
 DB 241 VLLTVIVIVITVQLPNIYKFCRAIDIIYSLTSCMSKRMIDAIQVETSIALFHSCLNP 300
 QY 301 ILVVFSGAFKQYVMKVAKKYSGMROROSVEEFPDSEGPTEPTSTFSI 350
 DB 301 ILVVFSGAFKQYVMKVAKKYSGMROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 10

ADA10754
 ID ADA10754 standard; protein; 350 AA.

AC ADA10754;

DT 06-NOV-2003 (first entry)

DE Human signal peptide containing protein SP-16 Incyte 2547007.

KW human; signal peptide-containing protein; cell proliferation disorder;

KW cell signaling disorder; Huntington's disease; stomach cancer;

KW uterine cancer; mucinous cystadenoma; arthritis; testicular seminoma;

KW prostate cancer; bladder cancer; renal cell cancer; schizophrenia;

KW asthma; cancer.

OS Homo sapiens.

PN US2003073162-A1.

PD 17-APR-2003.

PF 01-OCT-2001; 2001US-00968433.

PR 07-NOV-1997; 97US-00966316.

PR 17-MAR-1999; 99US-00271110.

PA (LALP/) LAL P. G.
 PA (AUTO/) AU-YOUNG J.
 PA (REDD/) REDDY R.
 PA (MURR/) MURRAY L. E.
 PA (MATH/) MATHUR P.

XX
 PI Lal PG, Au-Young J, Reddy R, Murry LE, Mathur P;
 DR WPI, 2003-567307/53.
 DR N-PSDB; ADA10755.
 PT New signal peptide-containing proteins and nucleic acids, useful in
 PT diagnosing, prognosing, treating or evaluating therapies for disorders
 PT associated with cell proliferation and cell signaling.
 PS Claim 1; Fig 1; 59pp; English.

XX
 XX The invention relates to a new purified signal peptide-containing
 CC protein. The signal peptide-containing proteins and nucleic acids
 CC encoding them are useful in diagnosing, prognosing, treating or
 CC evaluating therapies for disorders associated with cell proliferation and
 CC cell signaling such as Huntington's disease, stomach cancer, uterine
 CC cancer, mucinous cystadenoma, arthritis, testicular seminoma, prostate
 CC cancer, bladder cancer, renal cell cancer, schizophrenia, asthma and
 CC cancer. The nucleic acids may be used in hybridisation, amplification and
 CC screening technologies to identify and distinguish among the identical
 CC and related molecules in a sample and to produce transgenic cell lines or
 CC organisms which are model systems for cancers and upon which the toxicity
 CC and efficacy of potential therapeutic treatments may be tested. The
 CC present sequence represents the amino acid sequence of a human signal
 CC peptide containing protein.

SQ Sequence 350 AA;

Query Match 100.0%; Score 1819; DB 7; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLEQNSTDYEEENENGTVDYSQYELICKEDEVEPAKFLPVFLTIVFVIGLAGNS 60
 DB 1 MLEQNSTDYEEENENGTVDYSQYELICKEDEVEPAKFLPVFLTIVFVIGLAGNS 60
 QY 61 MVAIAYAYKKORTKTDVYILNLAVALDLLFTLPMAVNAVHGWLGKIMCKITSAALT 120
 DB 61 MVAIAYAYKKORTKTDVYILNLAVALDLLFTLPMAVNAVHGWLGKIMCKITSAALT 120
 QY 121 LNFVSGMOPACISIDRYAVAVTKVPSQSGVGKPCWIIICPCVMAAILLSIPOLVFYTVND 180
 DB 121 LNFVSGMOPACISIDRYAVAVTKVPSQSGVGKPCWIIICPCVMAAILLSIPOLVFYTVND 180
 QY 181 NARCIPIPPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIXISRPXK 240
 DB 181 NARCIPIPPRYLGTSMKALIQMLEICIGFVVPFLMGVCYFTARTLMKMPNIXISRPXK 240
 QY 241 VLLTVIVIVITVQLPNIYKFCRAIDIIYSLTSCMSKRMIDAIQVETSIALFHSCLNP 300
 DB 241 VLLTVIVIVITVQLPNIYKFCRAIDIIYSLTSCMSKRMIDAIQVETSIALFHSCLNP 300
 QY 301 ILVVFSGAFKQYVMKVAKKYSGMROROSVEEFPDSEGPTEPTSTFSI 350
 DB 301 ILVVFSGAFKQYVMKVAKKYSGMROROSVEEFPDSEGPTEPTSTFSI 350

RESULT 11

ADG19746
 ID ADG19746 standard; protein; 350 AA.

AC ADG19746;

DT 26-FEB-2004 (first entry)

DE Human G protein coupled receptor (GPCR) 2398.

KW cytostatic; nephrotoxic; antiinflammatory; cardiac; respiratory;
 KW gastrointestinal; neuroprotective; angiogenesis stimulator; gene therapy;
 KW 18636; 2466; 43238; 1983; 52881; 2398; 45449; 50287; 26908;
 KW cellular proliferative disorder; brain disorder; renal disorder;
 KW kidney disorder; inflammatory disorder; cardiovascular disorder;

KM liver disorder; intestinal disorder; respiratory disorder;
 KM angiosenic disorder; human; G protein coupled receptor; GPCR.
 OS Homo sapiens.
 FN US2003215860-A1.
 PD 20-NOV-2003.
 PF 03-APR-2003; 2003US-00407079.
 XX 29-FEB-2000; 2000US-0186059P.
 PR 24-MAR-2000; 2000US-0191845P.
 PR 22-MAY-2000; 2000US-0206019P.
 PR 17-NOV-2000; 2000US-00715790.
 PR 28-FEB-2001; 2001US-00796338.
 PR 22-MAY-2001; 2001US-00863200.
 PR 22-AUG-2001; 2001US-0314041P.
 PR 22-AUG-2001; 2001US-0314185P.
 PR 21-AUG-2002; 2002US-00225094.
 PR 22-AUG-2002; 2002US-00226102.
 PR 15-OCT-2002; 2002US-00272417.
 PR 29-OCT-2002; 2002US-00282837.
 XX (MILL-) MILLENNIUM PHARM INC.
 PA
 XX
 XX Glucksmann MA, Silos-Santiago I, Carroll JM, Galvin KM;
 PI WPI: 2004-010777/01.
 DR N-PSDB; ADG19745, ADG19747.
 XX
 XX New nucleic acid or polypeptide 18636, 2466, 43238, 1983, 52881, 2398,
 PT 45449, 50289, 52872 or 26908, useful in preparing a composition for
 PT treating e.g., cellular proliferative, brain, kidney, inflammatory or
 PT angiogenic disorder.
 XX
 PS Claim 4; SEQ ID NO 84; 163bp; English.
 XX
 XX The invention describes a new isolated 18636, 2466, 43238, 1983, 52881,
 CC 2398, 45449, 50289, 52872 or 26908 nucleic acid molecule comprising: a
 CC sequence comprising 939-1489 bp or its fragment comprising at least 15
 CC nucleotides; a sequence encoding a polypeptide comprising a sequence
 CC having 223-852 amino acids, or its allelic variant or fragment comprising
 CC at least 15 contiguous amino acids; or a sequence that hybridises with
 CC (1) under stringent conditions. The nucleic acid or polypeptide is useful
 CC in preparing a composition for treating a disorder characterised by
 CC aberrant 18636, 2466, 43238, 1983, 52881, 2398, 45449, 50289, 52872 or
 CC 26908 activity e.g., cellular proliferative, brain, renal, kidney,
 CC inflammatory, cardiovascular, liver, intestinal, respiratory or
 CC angiogenic disorder. This is the amino acid sequence of novel human
 CC protein 2398, a G protein coupled receptor (GPCR).
 XX
 SO Sequence 350 AA;
 Query Match 100.0%; Score 1819; DB 8; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALEONOSTDYEEENMNGTVDYSEYELICIKEDVREPAKVPFLPFLTIVFVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMNGTVDYSEYELICIKEDVREPAKVPFLPFLTIVFVIGLAGNS 60
 QY 61 MVAIAAYYKKORTKTDVYILNLAVADLLFLTPFMAVNAVHGWLGKIMKITSALYT 120
 DB 61 MVAIAAYYKKORTKTDVYILNLAVADLLFLTPFMAVNAVHGWLGKIMKITSALYT 120
 QY 121 LNFVSGMOFLACISIDRYAVATKVPQSQGVGRPCWIIICFVMAAAILISIPOLVFYTVND 180
 DB 121 LNFVSGMOFLACISIDRYAVATKVPQSQGVGRPCWIIICFVMAAAILISIPOLVFYTVND 180
 QY 181 NARCIPIPRRYGTSKAKALQMLEICIGVAVPPLINGVCYFTTARTLTKMPNPKISRPK 240
 DB 181 NARCIPIPRRYGTSKAKALQMLEICIGVAVPPLINGVCYFTTARTLTKMPNPKISRPK 240

QY 241 VLLTIVIVITVOTLPYNIIVKFCRAIDIIYSITSCNMSKRMIDIAIQVTESIALFHSCLNP 300
 DB 241 VLLTIVIVITVOTLPYNIIVKFCRAIDIIYSITSCNMSKRMIDIAIQVTESIALFHSCLNP 300
 QY 301 ILVYFMGASFQYVYKAKYKGSWROROSVSEEPFDSGPTEPTSTFSI 350
 DB 301 ILVYFMGASFQYVYKAKYKGSWROROSVSEEPFDSGPTEPTSTFSI 350
 RESULT 12
 ADM46693
 ID ADM46693 standard; protein; 350 AA.
 XX
 XX ADM46693;
 AC
 XX 03-JUN-2004 (first entry)
 DT
 XX Human chemokine receptor 11 protein.
 DE
 XX screening; therapeutic agent; peripheral; central nervous system;
 KM cardio-vascular disease; genitourinary; metabolic; haematological;
 KM chemokine receptor 11; CCR11; uropathic; antianaemic; human.
 XX
 XX Homo sapiens.
 OS
 XX
 XX EPI365245-A1.
 PN
 XX 26-NOV-2003.
 PD
 XX 23-MAY-2002; 2002EP-00011528.
 PF
 XX 23-MAY-2002; 2002EP-00011528.
 PR
 XX 23-MAY-2002; 2002EP-00011528.
 XX
 XX (FARB) BAYER AG.
 PA
 XX
 XX Golz S, Brueggemeier U, Geerts A;
 PI
 XX
 XX WPI: 2004-024617/03.
 DR N-PSDB; ADM46692.
 XX
 XX Screening for therapeutic agents useful for treating nervous system,
 PT cardiovascular, genitourinary, metabolic or hematological diseases in a
 PT mammal, by contacting a test compound with a chemokine receptor 11
 PT polypeptide.
 XX
 PS Disclosure; SEQ ID NO 2; 55bp; English.
 XX
 XX The invention relates to a novel method for screening for therapeutic
 CC agents useful for treating diseases. The diseases are chosen from
 CC disorders of peripheral and central nervous system, cardio-vascular
 CC diseases, genitourinary diseases, metabolic diseases and haematological
 CC diseases in mammals, by contacting a test compound with a chemokine
 CC receptor 11 (CCR11) polypeptide and detecting binding of the test
 CC compound to the CCR11 polypeptide. The therapeutic agents have uropathic
 CC and antianaemic activities. The invention comprises a further method
 CC useful for screening for therapeutic agents for treating the same
 CC diseases that act by binding to a CCR11 polynucleotide. A method is also
 CC provided for diagnosing the listed diseases. The compositions comprising
 CC identified therapeutic agents, or the CCR11 polypeptide or polynucleotide
 CC are useful for treating the diseases. This sequence represents the human
 CC chemokine receptor 11 protein of the invention.
 XX
 SO Sequence 350 AA;
 Query Match 100.0%; Score 1819; DB 8; Length 350;
 Best Local Similarity 100.0%; Pred. No. 1.1e-194;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MALEONOSTDYEEENMNGTVDYSEYELICIKEDVREPAKVPFLPFLTIVFVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMNGTVDYSEYELICIKEDVREPAKVPFLPFLTIVFVIGLAGNS 60

QY 61 MVAIAYKKORTKTDVYILNLAVALDLLFTLPMAVNAVHGVLGKIMCKITSALYT 120
 DB 61 MVAIAYKKORTKTDVYILNLAVALDLLFTLPMAVNAVHGVLGKIMCKITSALYT 120
 QY 121 LNFVSGMQLACISIDRYAVATKVPSSQSGVKPCWIIICFCVMAAILLSIPQLVFTYVD 180
 DB 121 LNFVSGMQLACISIDRYAVATKVPSSQSGVKPCWIIICFCVMAAILLSIPQLVFTYVD 180
 QY 181 NARCPIPFPRYIGTSMKALIQMLEICIGFVPLMGVCYFTTARTLMKMPNKRPRK 240
 DB 181 NARCPIPFPRYIGTSMKALIQMLEICIGFVPLMGVCYFTTARTLMKMPNKRPRK 240
 QY 241 VLLTVIVIVITQLPNIVKFCRAIDIIISLTSCMSKRMIDIAOVTSIALFHSCLNP 300
 DB 241 VLLTVIVIVITQLPNIVKFCRAIDIIISLTSCMSKRMIDIAOVTSIALFHSCLNP 300
 QY 301 ILYVFMGASFKNYVMKAKKYSWRQROSVBEPDSEGPTEPTSTFSI 350
 DB 301 ILYVFMGASFKNYVMKAKKYSWRQROSVBEPDSEGPTEPTSTFSI 350

RESULT 13

ADO29237
 ID ADO29237 standard; protein; 350 AA.

AC ADO29237;
 XX

DT 29-JUL-2004 (first entry)
 XX

DE Human GPCR CCR1, SEQ ID NO:338.
 XX

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;
 XX transgenic mouse; neurological disorder; adrenal gland disorder;
 XX colon disorder; intestinal disorder; cardiovascular disorder;
 XX muscular disorder; blood disorder; immune disorder; bone disorder;
 XX joint disorder; metabolic disorder; nutritive disorder; cancer;
 XX kidney disorder; liver disorder; lung disorder; breast disorder;
 XX ovary disorder; uterus disorder; prostate disorder; testis disorder;
 XX skin disorder; stomach disorder; pancreas disorder; spleen disorder;
 XX thymus disorder; thyroid disorder; antiparkinsonian; antineoplastic;
 XX cytostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;
 XX CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;
 XX diuretic; hepatotropic; antibacterial; antianemic; antiseborrhoeic;
 XX dermatological; antitumor; antihypertensive; antiallergic; anorectic;
 XX immunosuppressive; nephrotoxic; gene therapy; GPCR modulator; human;
 XX receptor.
 XX

XX Homo sapiens.
 OS

XX WO2004040000-A2.
 PN

XX 13-MAY-2004.
 PD

XX 09-SEP-2003; 2003WO-US028226.
 PF

XX 09-SEP-2002; 2002US-0409303P.
 PR

XX 09-APR-2003; 2003US-0461329P.
 PR

XX (PRIM-) PRIMAL INC.
 PA

XX Galanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;
 PI Madisen L, McIlwain KL, Pavlova MN, Vasiliadis D, Zeng H;
 XX

XX WPI; 2004-390329/36.
 DR

XX N-PSDB; ADO29837.
 DR

XX Novel mammalian G protein coupled receptors, useful for identifying
 PT compounds that modulates diagnosing and treating disease condition
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina
 PT pectoris, Parkinson's disease.
 XX

XX Claim 151; SEQ ID NO 338; 542pp; English.
 PS

CC The invention relates to human and mouse G protein-coupled receptors
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids
 CC of the invention; method of treating, preventing or diagnosing diseases
 CC associated with GPCRs of the invention; methods of screening for
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a
 CC mutation in a GPCR gene or in an endogenous GPCR gene; cells derived
 CC from the transgenic mice; kits comprising several mice, each of which has
 CC a mutation in a different GPCR gene of the invention; and kits comprising
 CC probes which hybridize to GPCR polynucleotides of the invention. The
 CC invention further discloses variants of the GPCR polypeptides and vectors
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may
 CC be used in the diagnosis, treatment or prevention of a wide variety of
 CC diseases including neurological disorders (e.g., Alzheimer's disease,
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);
 CC disorders of the adrenal gland; disorders of the colon or intestine
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and
 CC thyroid (e.g., cancers). The present sequence represents a GPCR of the
 CC invention. Note: The full sequence data for this patent did not form part
 CC of the printed specification; those sequences not shown were obtained in
 CC electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pcr_sequences.
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RESULT 14

ADRO3495
 ID ADRO3495 standard; protein; 378 AA.

XX ADRO3495;
 AC

XX 21-OCT-2004 (first entry)
 DT

XX Novel human cytokine receptor CCX CR.
 XX

KW antiallergic; antiinflammatory; antimicrobial; cyostatic;
 KW immunostimulant; immunosuppressive; CCX chemokine receptor; CCX CKR;
 KW EB11-ligand chemokine; ELC; secondary lymphoid-tissue chemokine; SLC;
 KW thymus-expressed chemokine; TECK; chemokine binding activity;
 KW CCX CKR modulator; chemokine binding modulator; inflammation; allergy;
 KW autoimmune disease; graft rejection; cancer; infectious disease;
 KW immunosuppressive disease; human; receptor.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 350..352
 FT /note= "Encoded by ATTTAAAGTAAAC"
 FT Misc-difference 362..363
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 XX
 PD 29-JUL-2004.
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 PE 24-FEB-2004; 2004US-00787018.
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 PR 20-DEC-1999; 99US-0172979P.
 PR 28-DEC-1999; 99US-0173388P.
 PR 03-MAR-2000; 2000US-0186626P.
 PR 10-OCT-2000; 2000US-00686019.
 PR 21-NOV-2000; 2000US-00721495.
 XX
 PA (CHEM-) CHEMOCENTRIX INC.
 XX
 PI Gosling J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;
 XX WPI; 2004-561394/54.
 DR N-PSDB; ADR03494.
 XX
 PT New CCX chemokine receptor polypeptide that binds ELC, SLC or TECK,
 PT useful in identifying modulators of its expression or activity which are
 PT potentially useful for treating inflammation, allergies, autoimmune
 PT disease and cancer.
 FT
 FT Claim 2; SEQ ID NO 2; 37bp; English.
 PS
 XX
 CC The invention describes an isolated or recombinant CCX chemokine receptor
 CC (CCX CKR) polypeptide (1) or its fragment that binds EB11-ligand
 CC chemokine (ELC), Secondary lymphoid-tissue chemokine (SLC) or thymus-
 CC expressed chemokine (TECK). Also described are: a fusion protein
 CC comprising the polypeptide; an isolated polynucleotide encoding (1) or
 CC its fragment; an isolated polynucleotide comprising a sequence encoding a
 CC polypeptide that has a chemokine binding activity which is: a
 CC polynucleotide comprising the sequence of SEQ ID NO:1 or SEQ ID NO:3; a
 CC polynucleotide that hybridises under stringent conditions to (a); or a
 CC polynucleotide sequence which is degenerate as a result of the genetic
 CC code to the sequences defined in (a) or (b); a recombinant (expression)
 CC vector comprising the polynucleotide; a host cell comprising the vector;
 CC producing a CCX CKR protein, peptide or fusion protein; a polynucleotide
 CC primer, probe, antisense oligonucleotide or ribozyme comprising at least
 CC 15 contiguous bases identical or exactly complementary to the 147-bp
 CC sequence; an antibody or its fragment that specifically binds to the
 CC polypeptide; an isolated cell capable of secreting the antibody; a
 CC hybridoma capable of secreting the antibody; detecting a CCX CKR gene
 CC product in a sample; amplifying a CCX CKR polynucleotide in a sample;
 CC identifying a modulator of the binding of CCX CKR to a chemokine;
 CC producing a pharmaceutical composition from a modulator of CCX CKR
 CC (chemokine binding) activity; identifying a modulator of CCX CKR activity
 CC ; and treating a CCX CKR-mediated condition in a mammal. Agents that
 CC modulate the activity of CCX CKR in a cell or tissue in an animal are
 CC useful for treating CCX CKR related conditions such as inflammation,
 CC allergy, an autoimmune disease, graft rejection, cancer, an infectious
 CC disease or an immunosuppressive disease, preferably inflammation. This is

CC the amino acid sequence of novel chemokine receptor CCX CKR.
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 ID AAB62389 standard; protein; 382 AA.
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 AC AAB62389;
 XX
 DT 29-JUN-2001 (first entry)
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 DE Human chemokine receptor CCX CKR polypeptide.
 XX
 KW Chemokine receptor; CCX CKR; chemokine; ELC; SLC; TECK; modulator;
 KW antiinflammatory; immunosuppressive; cyostatic; antiallergic; human;
 KW immunostimulant; gene therapy.
 OS
 XX Homo sapiens.
 FH Key Location/Qualifiers
 FT Misc-difference 351
 FT /note= "encoded by TAA"
 FT Misc-difference 353
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 FT Misc-difference 371
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 PD 19-APR-2001.
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 PF 10-OCT-2000; 2000MO-US028067.
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 PR 28-DEC-1999; 99US-0173389P.
 PR 03-MAR-2000; 2000US-0186626P.
 XX
 PA (CHEM-) CHEMOCENTRIX INC.
 XX

PI Gosling J, Dairaghi DJ, Hanley M, Miao Z, Talbot D, Schall TJ;
 XX
 DR WPI; 2001-281975/29.
 DR N-PSDB; AAF57685.

XX Isolated or recombinant chemokine receptor (designated CCX CKR)
 PT polypeptide (PI) or its fragment, useful for identifying CCX CKR
 PT modulators which can be used in the treatment of inflammation, allergy,
 PT an autoimmune disease or cancer.

XX Claim 4; Fig 1; 72pp; English.

XX The invention relates to an isolated or recombinant chemokine receptor
 CC designated CCX CKR) polypeptide which binds to chemokines such as RLC,
 CC SLK or TECK. The CCX CKR polypeptide is useful for identifying CCX CKR
 CC modulators. An agent that modulates the activity or expression of CCX CKR
 CC in a cell or tissue in the mammal is useful in the treatment of a CCX CKR
 CC -mediated condition such as inflammation, allergy, an autoimmune disease,
 CC graft rejection, cancer, an infectious disease or an immunosuppressive
 CC disease. The present sequence represents the human CCX CKR polypeptide

XX Sequence 382 AA;

Query Match 100.0%; Score 1819; DB 4; Length 382;

Best Local Similarity 100.0%; Pred. No. 1.2e-194;

Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 DB 121 LNFVSGMOFLACISIDRYAVATKVPQSQGVGKPCWIIICFCVMAAAILLSIPQLVFTYVND 180
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Job time : 84 secs

GenCore version 5.1.6
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(without alignments)
850.486 Million cell updates/sec

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1819	100.0	350	US-09-765-994-2	Sequence 2, Appl1
2	1819	100.0	350	US-09-796-338A-8	Sequence 8, Appl1
3	1819	100.0	350	US-09-966-433-16	Sequence 16, Appl1
4	1819	100.0	350	US-10-282-837-8	Sequence 8, Appl1
5	1819	100.0	350	US-10-225-567A-607	Sequence 607, App
6	1819	100.0	350	US-10-288-222A-10	Sequence 10, Appl1
7	1819	100.0	350	US-10-145-586-8	Sequence 8, Appl1
8	1819	100.0	350	US-10-239-423-75	Sequence 75, Appl1
9	1819	100.0	350	US-10-407-079-84	Sequence 84, Appl1
10	1814	99.7	349	US-09-765-994-4	Sequence 4, Appl1
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16	1810	99.5	350	US-10-417-807A-24	Sequence 24, Appl1
17	1810	99.5	350	US-10-723-955-74	Sequence 74, Appl1
18	1810	99.5	350	US-10-782-596-22	Sequence 22, Appl1
19	1803	99.1	350	US-09-910-695-8	Sequence 8, Appl1
20	1620	89.1	350	US-09-968-433-79	Sequence 79, Appl1
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22	862	47.4	164	US-10-276-774-1532	Sequence 1532, App
23	761	41.8	175	US-09-764-893-91	Sequence 91, Appl1
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ALIGNMENTS

RESULT 1	US-09-765-994-2	Application US/09765994
1	Sequence 2, Appl1	US/09765994
2	Patent No. US20010016336A1	
3	GENERAL INFORMATION:	
4	APPLICANT: ELLIS, CATHERINE	
5	TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR	
6	FILE REFERENCE: GH-70225-C1	
7	CURRENT APPLICATION NUMBER: US/09/765,994	
8	CURRENT FILING DATE: 2001-01-19	
9	PRIOR APPLICATION NUMBER: 60/055,895	
10	PRIOR FILING DATE: 1997-08-15	
11	PRIOR APPLICATION NUMBER: 08/962,922	
12	PRIOR FILING DATE: 1997-10-27	
13	NUMBER OF SEQ ID NOS: 4	
14	SOFTWARE: FaastSeq for Windows Version 3.0	
15	SEQ ID NO 2	
16	LENGTH: 350	
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18	ORGANISM: HOMO SAPIENS	
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; Patent No. US20020061522A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/09/796,338A
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; NUMBER OF SEQ ID NOS: 26
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RESULT 3
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; Sequence 16, Application US/09968433
; Patent No. US20030073162A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Vanice

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; APPLICANT: Reddy, Roopa
; APPLICANT: Murry, Lynn E.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE-CONTAINING PROTEINS
; FILE REFERENCE: PC-0051 CIP
; CURRENT APPLICATION NUMBER: US/09/968,433
; CURRENT FILING DATE: 2001-10-01
; NUMBER OF SEQ ID NOS: 79
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; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; TITLE OF INVENTION: 1983, 52881, 2398, 45449, 50289, AND
; FILE REFERENCE: 10448-020001
; CURRENT APPLICATION NUMBER: US/10/282,837
; PRIOR FILING DATE: 2002-10-29
; PRIOR APPLICATION NUMBER: US/09/796,338
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: US 60/186,059
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-282-837-8

```

```

Query Match      100.0%; Score 1819; DB 14; Length 350;
Best Local Similarity 100.0%; Pred. No. 9.7e-152;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDYREPAKVPFLPVFLTIVFVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDYREPAKVPFLPVFLTIVFVIGLAGNS 60
 QY 61 MVVAIYAAYKKORTKTDDVYILNLAVADLLFLTPPMVAVNAVHGVWLGIMCKITISALYT 120
 DB 61 MVVAIYAAYKKORTKTDDVYILNLAVADLLFLTPPMVAVNAVHGVWLGIMCKITISALYT 120
 QY 121 LNFVSGMOPLACISIDRYAVATKVPQSOGVGCPCWIIICFCVMAAAILLSIPOLVFTYVND 180
 DB 121 LNFVSGMOPLACISIDRYAVATKVPQSOGVGCPCWIIICFCVMAAAILLSIPOLVFTYVND 180
 QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKMPNKRISRLK 240
 DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKMPNKRISRLK 240
 QY 241 VLLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 DB 241 VLLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 QY 301 ILYVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350
 DB 301 ILYVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350

RESULT 5
 US-10-225-567A-607
 Sequence 607, Application US/10225567A
 Publication No. US20030113798A1
 GENERAL INFORMATION:

APPLICANT: Lifespan Biosciences
 APPLICANT: Brown, Joseph P.
 APPLICANT: Burmer, Glenna C.
 APPLICANT: Roush, Christine L.
 TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
 FILE REFERENCE: 1920-4-4
 CURRENT APPLICATION NUMBER: US/10/225,567A
 CURRENT FILING DATE: 2001-12-19
 PRIOR APPLICATION NUMBER: 60/257,144
 PRIOR FILING DATE: 2000-12-19
 NUMBER OF SEQ ID NOS: 2292
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 607
 LENGTH: 350
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-225-567A-607

Query Match 100.0%; Score 1819; DB 14; Length 350;
 Best Local Similarity 100.0%; Pred. No. 9.7e-152;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDYREPAKVPFLPVFLTIVFVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDYREPAKVPFLPVFLTIVFVIGLAGNS 60
 QY 61 MVVAIYAAYKKORTKTDDVYILNLAVADLLFLTPPMVAVNAVHGVWLGIMCKITISALYT 120
 DB 61 MVVAIYAAYKKORTKTDDVYILNLAVADLLFLTPPMVAVNAVHGVWLGIMCKITISALYT 120
 QY 121 LNFVSGMOPLACISIDRYAVATKVPQSOGVGCPCWIIICFCVMAAAILLSIPOLVFTYVND 180
 DB 121 LNFVSGMOPLACISIDRYAVATKVPQSOGVGCPCWIIICFCVMAAAILLSIPOLVFTYVND 180
 QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKMPNKRISRLK 240
 DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKMPNKRISRLK 240
 QY 241 VLLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 DB 241 VLLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300

QY 301 ILYVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350
 DB 301 ILYVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350

RESULT 6
 US-10-288-222A-10
 Sequence 10, Application US/10288222A
 Publication No. US20030119742A1
 GENERAL INFORMATION:

APPLICANT: Logan, Thomas Joseph
 APPLICANT: Galvin, Katherine
 APPLICANT: Chun, Mayoung
 TITLE OF INVENTION: Methods and Compositions to treat
 TITLE OF INVENTION: Cardiovascular Disease Using 139, 258, 1261, 1486, 2398, 2414,
 FILE REFERENCE: MP12001-286PIR(M)
 CURRENT APPLICATION NUMBER: US/10/288,222A
 CURRENT FILING DATE: 2002-11-05
 NUMBER OF SEQ ID NOS: 30
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 10
 LENGTH: 350
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-288-222A-10

Query Match 100.0%; Score 1819; DB 14; Length 350;
 Best Local Similarity 100.0%; Pred. No. 9.7e-152;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDYREPAKVPFLPVFLTIVFVIGLAGNS 60
 DB 1 MALEONOSTDYEEENMGTYDYSOYELICIKEDYREPAKVPFLPVFLTIVFVIGLAGNS 60
 QY 61 MVVAIYAAYKKORTKTDDVYILNLAVADLLFLTPPMVAVNAVHGVWLGIMCKITISALYT 120
 DB 61 MVVAIYAAYKKORTKTDDVYILNLAVADLLFLTPPMVAVNAVHGVWLGIMCKITISALYT 120
 QY 121 LNFVSGMOPLACISIDRYAVATKVPQSOGVGCPCWIIICFCVMAAAILLSIPOLVFTYVND 180
 DB 121 LNFVSGMOPLACISIDRYAVATKVPQSOGVGCPCWIIICFCVMAAAILLSIPOLVFTYVND 180
 QY 181 NARCIPIPRYIGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKMPNKRISRLK 240
 DB 181 NARCIPIPRYIGTSMKALIQMLEICIGFVPPFLMGVCYFTARTLMKMPNKRISRLK 240
 QY 241 VLLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 DB 241 VLLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCMSKMDIAIQVTSIALFHSCLNP 300
 QY 301 ILYVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350
 DB 301 ILYVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEGPTEPSTFSI 350

RESULT 7
 US-10-145-586-8
 Sequence 8, Application US/10145586
 Publication No. US20030138890A1
 GENERAL INFORMATION:
 APPLICANT: Alexandra Gluckemann, Maria
 APPLICANT: Silos-Santlago, Immaculada
 APPLICANT: M. Galvin, Katherine
 APPLICANT: Welch, Nadine
 APPLICANT: Curtis, Roy A. J.
 APPLICANT: Bandaru, Rajasekhar
 APPLICANT: Kapeller-Libermann, Rosana
 TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTOR FAMILY MEMBERS,
 TITLE OF INVENTION: HUMAN THIOREDOXIN FAMILY MEMBERS, HUMAN LECTIN-RICH
 TITLE OF INVENTION: REPEAT FAMILY MEMBERS, AND HUMAN RINGFINGER FAMILY MEMBER
 FILE REFERENCE: 10448-188001
 CURRENT APPLICATION NUMBER: US/10/145,586

Db 1 MALEONOSTDYEEENMGTYDYSQYELICIKEDVREPAKVLVPLFTIVFVIGLAGNS 60
 Qy 61 MVAIYAYKKORTKTDVYILNLAVADLLFTLPFWANVAHGWVLGKIMCKITSALT 120
 Db 61 MVAIYAYKKORTKTDVYILNLAVADLLFTLPFWANVAHGWVLGKIMCKITSALT 120
 Qy 121 INFVSGMOPLACISIDRYAVATKVPSSQGVKPCWIIICFCVMAAIIILSIPOLVFYTVND 180
 Db 121 INFVSGMOPLACISIDRYAVATKVPSSQGVKPCWIIICFCVMAAIIILSIPOLVFYTVND 180
 Qy 181 NARCIPIPRYLGTSKMAIIQMLEICIGFVPPFLIMGVCFITARTLMKPNIKISRLPX 240
 Db 181 NARCIPIPRYLGTSKMAIIQMLEICIGFVPPFLIMGVCFITARTLMKPNIKISRLPX 240
 Qy 241 VLTIVIVFIVTOLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQTESIALFHSCLNP 300
 Db 241 VLTIVIVFIVTOLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQTESIALFHSCLNP 300
 Qy 301 ILYVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEPTSTFSI 350
 Db 301 ILYVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEPTSTFSI 350

RESULT 10

US-09-765-994-4
 ; Sequence 4, Application US/09765994
 ; Patent No. US20010016336A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ELLIS, CATHERINE
 ; TITLE OF INVENTION: THE G-PROTEIN COUPLED RECEPTOR
 ; FILE REFERENCE: GH-70225-CI
 ; CURRENT APPLICATION NUMBER: US/09/765,994
 ; CURRENT FILING DATE: 2001-01-19
 ; PRIOR APPLICATION NUMBER: 60/055,895
 ; PRIOR FILING DATE: 1997-08-15
 ; PRIOR APPLICATION NUMBER: 08/962,922
 ; PRIOR FILING DATE: 1997-10-27
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FaSTSeq for Windows Version 3.0
 ; SEQ ID NO 4
 ; LENGTH: 349
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-765-994-4

Query Match 99.7%; Score 1814; DB 9; Length 349;
 Best Local Similarity 100.0%; Pred. No. 2,7e-151;
 Matches 349; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 ALEONOSTDYEEENMGTYDYSQYELICIKEDVREPAKVLVPLFTIVFVIGLAGNS 61
 Db 1 ALEONOSTDYEEENMGTYDYSQYELICIKEDVREPAKVLVPLFTIVFVIGLAGNS 60
 Qy 62 VVAIYAYKKORTKTDVYILNLAVADLLFTLPFWANVAHGWVLGKIMCKITSALT 121
 Db 61 VVAIYAYKKORTKTDVYILNLAVADLLFTLPFWANVAHGWVLGKIMCKITSALT 120
 Qy 122 INFVSGMOPLACISIDRYAVATKVPSSQGVKPCWIIICFCVMAAIIILSIPOLVFYTVND 181
 Db 122 INFVSGMOPLACISIDRYAVATKVPSSQGVKPCWIIICFCVMAAIIILSIPOLVFYTVND 180
 Qy 181 NARCIPIPRYLGTSKMAIIQMLEICIGFVPPFLIMGVCFITARTLMKPNIKISRLPX 241
 Db 181 NARCIPIPRYLGTSKMAIIQMLEICIGFVPPFLIMGVCFITARTLMKPNIKISRLPX 240
 Qy 242 LTVIVIVFIVTOLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQTESIALFHSCLNP 301
 Db 241 LTVIVIVFIVTOLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQTESIALFHSCLNP 300
 Qy 302 ILYVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEPTSTFSI 350
 Db 301 ILYVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEPTSTFSI 349

RESULT 11
 US-10-403-161-12
 ; Sequence 12, Application US/10403161
 ; Publication No. US20040043930A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, David et al.
 ; TITLE OF INVENTION: NOVEL PROTEINS AND NUCLEIC ACIDS ENCODING SAME
 ; FILE REFERENCE: 21402-573C
 ; CURRENT APPLICATION NUMBER: US/10/403,161
 ; CURRENT FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: 60/370349
 ; PRIOR FILING DATE: 2002-04-05
 ; PRIOR APPLICATION NUMBER: 60/384543
 ; PRIOR FILING DATE: 2002-05-30
 ; PRIOR APPLICATION NUMBER: 60/370969
 ; PRIOR FILING DATE: 2002-04-08
 ; PRIOR APPLICATION NUMBER: 60/403748
 ; PRIOR FILING DATE: 2002-06-15
 ; PRIOR APPLICATION NUMBER: 60/372019
 ; PRIOR FILING DATE: 2002-04-12
 ; PRIOR APPLICATION NUMBER: 60/374379
 ; PRIOR FILING DATE: 2002-04-22
 ; PRIOR APPLICATION NUMBER: 09/779679
 ; PRIOR FILING DATE: 2001-02-08
 ; PRIOR APPLICATION NUMBER: 60/181045
 ; PRIOR FILING DATE: 2000-02-08
 ; PRIOR APPLICATION NUMBER: 10/055877
 ; PRIOR FILING DATE: 2002-01-22
 ; PRIOR APPLICATION NUMBER: 60/262892
 ; Remaining Prior Application data removed - See file wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 173
 ; SOFTWARE: CuroSeqList version 0.1
 ; SEQ ID NO 12
 ; LENGTH: 348
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-403-161-12

Query Match 99.5%; Score 1810; DB 15; Length 348;
 Best Local Similarity 100.0%; Pred. No. 6e-151;
 Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LEONOSTDYEEENMGTYDYSQYELICIKEDVREPAKVLVPLFTIVFVIGLAGNS 62
 Db 1 LEONOSTDYEEENMGTYDYSQYELICIKEDVREPAKVLVPLFTIVFVIGLAGNS 60
 Qy 63 VVAIYAYKKORTKTDVYILNLAVADLLFTLPFWANVAHGWVLGKIMCKITSALT 122
 Db 61 VVAIYAYKKORTKTDVYILNLAVADLLFTLPFWANVAHGWVLGKIMCKITSALT 120
 Qy 123 FVSGMOPLACISIDRYAVATKVPSSQGVKPCWIIICFCVMAAIIILSIPOLVFYTVND 182
 Db 123 FVSGMOPLACISIDRYAVATKVPSSQGVKPCWIIICFCVMAAIIILSIPOLVFYTVND 180
 Qy 181 NARCIPIPRYLGTSKMAIIQMLEICIGFVPPFLIMGVCFITARTLMKPNIKISRLPX 242
 Db 181 NARCIPIPRYLGTSKMAIIQMLEICIGFVPPFLIMGVCFITARTLMKPNIKISRLPX 240
 Qy 243 LTVIVIVFIVTOLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQTESIALFHSCLNP 302
 Db 241 LTVIVIVFIVTOLPYNIVKFCRAIDIIYSLITSCMSKMDIAIQTESIALFHSCLNP 300
 Qy 303 ILYVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEPTSTFSI 350
 Db 301 ILYVFMGASFKNYVMKAKKYGSMROROSVEEFPDSEPTSTFSI 348

RESULT 12
 US-09-875-076-22
 ; Sequence 22, Application US/09875076

```
/ Publication No. US20030017528A1
/ GENERAL INFORMATION:
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Liaw, Chen W.
/ APPLICANT: Lin, I-Lin
/ TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
/ FILE REFERENCE: AREN0050
/ CURRENT APPLICATION NUMBER: US/09/875,076
/ CURRENT FILING DATE: 2001-06-06
/ PRIOR APPLICATION NUMBER: 09/417,044
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,851
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,127
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,131
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/141,448
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 60/156,653
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,633
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,555
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,634
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/157,280
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,294
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,281
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,293
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,282
/ PRIOR FILING DATE: 1999-10-01
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 350
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-875-076-22

Query Match          99.5%; Score 1810; DB 10; Length 350;
Best Local Similarity 99.4%; Pred. No. 6e-151;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      1 MALEONQSDYDYEEENEMNGTIDYISQYELICIKEDYREPAKVLPPVFLTIYVYIGLAGNS 60
      11 |||||
DB      1 MALEONQSDYDYEEENEMNGTIDYISQYELICIKEDYREPAKVLPPVFLTIYVYIGLAGNS 60
      11 |||||
QY      61 MVAIAYYKKQKTKTDVYILNLAVDLLFTLPFAVNAVHGWGLGKIMCKITSALYI 120
      61 |||||
DB      61 MVAIAYYKKQKTKTDVYILNLAVDLLFTLPFAVNAVHGWGLGKIMCKITSALYI 120
      61 |||||
QY      121 LNFVSGMOFLACISIDRYVAATVTKVPSQSGVGKPCWIIICFVMAAILISIPQLVFYTVND 180
      121 |||||
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DB      121 LNFVSGMOFLACISIDRYVAATVTKVPSQSGVGKPCWIIICFVMAAILISIPQLVFYTVND 180
      121 |||||
QY      181 NARCIPIPRYIGTSMKLLIOWLEICIGFVVPFLMGVCYFTTATLTKMPPIKISRPBK 240
      181 |||||
DB      181 NARCIPIPRYIGTSMKLLIOWLEICIGFVVPFLMGVCYFTTATLTKMPPIKISRPBK 240
      181 |||||
QY      241 VLLTVIVFIYVTLQPLPYNIVKFCRAIDIIYSLLTSCNMSKMDIAIQVESIALFHSCLNP 300
      241 |||||
DB      241 VLLTVIVFIYVTLQPLPYNIVKFCRAIDIIYSLLTSCNMSKMDIAIQVESIALFHSCLNP 300
      241 |||||
QY      301 ILVFMGASFKNYVVKVAKKTSWRRORSVEEFPDSBGPTEPSTESI 350
      301 |||||
DB      301 ILVFMGASFKNYVVKVAKKTSWRRORSVEEFPDSBGPTEPSTESI 350
      301 |||||

RESULT 13
US-09-876-252-24
/ Sequence 24, Application US/09876252
/ Publication No. US20030018182A1
/ GENERAL INFORMATION:
/ APPLICANT: Behan, Dominic P.
/ APPLICANT: Lehmann-Brunema, Karin
/ APPLICANT: Chalmers, Derek T.
/ APPLICANT: Lowitz, Kevin P.
/ APPLICANT: Lin, I-Lin
/ APPLICANT: Dang, Huong T.
/ APPLICANT: Chen, Ruoping
/ APPLICANT: Liaw, Chen W.
/ TITLE OF INVENTION: Non-Endogenous Constititively Activated Human G Protein Coupled Rec
/ FILE REFERENCE: AREN-0054
/ CURRENT APPLICATION NUMBER: US/09/876,252
/ CURRENT FILING DATE: 2001-06-07
/ PRIOR APPLICATION NUMBER: 09/416,760
/ PRIOR FILING DATE: 1999-10-12
/ PRIOR APPLICATION NUMBER: 09/170,496
/ PRIOR FILING DATE: 1998-10-13
/ PRIOR APPLICATION NUMBER: 60/110,060
/ PRIOR FILING DATE: 1998-11-27
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,852
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/109,213
/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/123,944
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,945
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,948
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,951
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: 60/108,029
/ PRIOR FILING DATE: 1998-11-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,127
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/137,131
/ PRIOR FILING DATE: 1999-05-28
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; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: Patentln version 3.0
; SEQ ID NO 24
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-252-24

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Query Match      99.5%; Score 1810; DB 10; Length 350;
Best Local Similarity 99.4%; Pred. No. 6e-151;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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QY      1 MLEQNOSTDYEEENENGTGYDYOYELICKEDEVEPAKYFLPVFLTIIVFVIGLAGNS 60
DB      1 MLEQNOSTDYEEENENGTGYDYOYELICKEDEVEPAKYFLPVFLTIIVFVIGLAGNS 60
QY      61 MVAIYAAYKKORTKTIDYIILNLAVALDLLFTLPFMAVNAVHGWLGKIMCKITSALYT 120
DB      61 MVAIYAAYKKORTKTIDYIILNLAVALDLLFTLPFMAVNAVHGWLGKIMCKITSALYT 120
QY      121 LNFVSGMOPLACISIDRYAAVTKVPSQSGVGKPCWIIICVMAAALLSIPLVFTYVND 180
DB      121 LNFVSGMOPLACISIDRYAAVTKVPSQSGVGKPCWIIICVMAAALLSIPLVFTYVND 180
QY      181 NARCIPIPRYIGTSMKALIQMLEICIGFVPEFLMGVCYFTTARTLMKMPNIKISRPLK 240
DB      181 NARCIPIPRYIGTSMKALIQMLEICIGFVPEFLMGVCYFTTARTLMKMPNIKISRPLK 240
QY      241 VLLTVIVIVTQLPYNIVKFCRAIDIIYSLITSCKMSKMDIAIQVTSIALFHSCLNP 300
DB      241 VLLTVIVIVTQLPYNIVKFCRAIDIIYSLITSCKMSKMDIAIQVTSIALFHSCLNP 300
QY      301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVVEFPDSEGPTEPTSTFSI 350
DB      301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVVEFPDSEGPTEPTSTFSI 350

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RESULT 14

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US-10-272-983-22
; Sequence 22, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213

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; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See file wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 22
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-272-983-22

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Query Match      99.5%; Score 1810; DB 14; Length 350;
Best Local Similarity 99.4%; Pred. No. 6e-151;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB      181 NARCIPIPRYIGTSMKALIQMLEICIGFVPEFLMGVCYFTTARTLMKMPNIKISRPLK 240
QY      241 VLLTVIVIVTQLPYNIVKFCRAIDIIYSLITSCKMSKMDIAIQVTSIALFHSCLNP 300
DB      241 VLLTVIVIVTQLPYNIVKFCRAIDIIYSLITSCKMSKMDIAIQVTSIALFHSCLNP 300
QY      301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVVEFPDSEGPTEPTSTFSI 350
DB      301 ILYVFMGASFKNYVMKVAKKYSGWRQROSVVEFPDSEGPTEPTSTFSI 350

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RESULT 15

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US-10-393-807-22
; Sequence 22, Application US/10393807
; Publication No. US20030175891A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/393,807
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416

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/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121, 851
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/123, 946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123, 949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/136, 436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136, 437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136, 439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136, 567
/ PRIOR FILING DATE: 1999-05-28
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 350
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-393-807-22

Query Match 99.5%; Score 1810; DB 14; Length 350;
Best Local Similarity 99.4%; Pred. No. 6e-151;
Matches 348; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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DB 241 VLLTVIVIVTQLPYNIVKFCRAIDIIYSLITSCKMSKMDIAIQVTESIALFHSCLNP 300
QY 301 ILYVFMGASFKNYVMKVAKKYGSWRQROSVBEFPDSEGPTEPTSTPSI 350
DB 301 ILYVFMGASFKNYVMKVAKKYGSWRQROSVBEFPDSEGPTEPTSTPSI 350

Search completed: March 2, 2005, 04:34:39
Job time : 137 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 04:18:17 ; Search time 22 Seconds
(without alignments)
1187.599 Million cell updates/sec

Title: US-09-721-341-2

Perfect score: 1819

Sequence: 1 MALAEQNQSDYYEENEMNG.....VEEPDSESGPTPTSTFST 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:*

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Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	2	US-08-966-316-16 Sequence 16, Appl
2	1819	100.0	350	4	US-09-721-908-2 Sequence 2, Appl
3	1819	100.0	350	4	US-09-721-341-2 Sequence 2, Appl
4	1819	100.0	350	4	US-09-721-495B-2 Sequence 2, Appl
5	1808	99.4	350	4	US-09-556-002-2 Sequence 2, Appl
6	1803	99.1	350	4	US-09-910-695-8 Sequence 8, Appl
7	1620	89.1	350	2	US-08-966-316-18 Sequence 18, Appl
8	659	36.2	358	3	US-08-153-848-19 Sequence 19, Appl
9	659	36.2	358	3	US-09-299-843A-19 Sequence 19, Appl
10	659	36.2	358	3	US-09-088-337B-19 Sequence 19, Appl
11	659	36.2	358	5	PCT-US93-11153-19 Sequence 19, Appl
12	659	36.2	378	1	US-08-153-848-15 Sequence 15, Appl
13	659	36.2	378	3	US-09-299-843A-15 Sequence 15, Appl
14	659	36.2	378	3	US-09-251-545-1 Sequence 1, Appl
15	659	36.2	378	3	US-09-088-337B-15 Sequence 15, Appl
16	659	36.2	378	4	US-09-170-496D-74 Sequence 74, Appl
17	659	36.2	378	5	PCT-US93-11153-15 Sequence 15, Appl
18	659	36.2	410	1	US-08-153-848-7 Sequence 7, Appl
19	659	36.2	410	3	US-09-299-843A-7 Sequence 7, Appl
20	659	36.2	410	3	US-09-088-337B-7 Sequence 7, Appl
21	659	36.2	410	5	PCT-US93-11153-7 Sequence 7, Appl
22	655	36.0	378	4	US-09-170-496D-204 Sequence 204, App
23	650	35.7	378	3	US-09-299-843A-66 Sequence 66, Appl
24	650	35.7	378	3	US-09-088-337B-66 Sequence 66, Appl
25	643	35.3	369	4	US-09-721-341-6 Sequence 6, Appl
26	643	35.3	369	4	US-09-721-495B-6 Sequence 6, Appl
27	643	35.3	371	4	US-09-949-016-11223 Sequence 11223, A

28	643	35.3	378	1	US-08-383-750-2 Sequence 2, Appl
29	643	35.3	378	1	US-08-383-751A-2 Sequence 2, Appl
30	643	35.3	378	3	US-08-352-678-2 Sequence 2, Appl
31	643	35.3	378	3	US-09-045-583-49 Sequence 49, Appl
32	643	35.3	378	4	US-09-534-185-49 Sequence 49, Appl
33	643	35.3	378	4	US-09-536-954-2 Sequence 2, Appl
34	643	35.3	378	4	US-09-929-583B-2 Sequence 2, Appl
35	643	35.3	378	4	US-09-721-341-7 Sequence 7, Appl
36	643	35.3	378	5	PCT-US93-09636-2 Sequence 2, Appl
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38	637	35.0	357	3	US-09-266-464-2 Sequence 2, Appl
39	637	35.0	357	4	US-09-170-496D-24 Sequence 24, Appl
40	637	35.0	357	4	US-09-952-385-2 Sequence 2, Appl
41	637	35.0	369	4	US-09-826-509-481 Sequence 481, App
42	635.5	34.9	359	1	US-08-153-848-24 Sequence 24, Appl
43	635.5	34.9	359	3	US-09-299-843A-24 Sequence 24, Appl
44	635.5	34.9	359	3	US-09-088-337B-24 Sequence 24, Appl
45	635.5	34.9	359	5	PCT-US93-11153-24 Sequence 24, Appl

ALIGNMENTS

RESULT 1
US-08-966-316-16
; Sequence 16, Application US/08966316
; Patent No. 5932445
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; APPLICANT: Au-Young, Janice
; APPLICANT: Reddy, Roopa
; APPLICANT: Murty, Lynn B.
; APPLICANT: Mathur, Preete
; TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: IBM Compatible
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/966,316
; FILING DATE: Herewith
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0424 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 350 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: UTRSN0T11
; CLONE: 2547002
US-08-966-316-16

Query Match 100.0%; Score 1819; DB 2; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 301 ILYVFGASFKNYVMKAKKYGSMROROSVEEPFDSGPTSTFSI 350

RESULT 2

US-09-721-908-2
Sequence 2, Application US/09721908
Patent No. 6699677
GENERAL INFORMATION:
APPLICANT: Schall, Thomas J.
APPLICANT: Talbot, Dale
APPLICANT: Zhenhua, Miao
APPLICANT: Zheng, Wei
APPLICANT: Chemocentryx, Inc.
TITLE OF INVENTION: Tethered Ligands and Methods of Use
FILE REFERENCE: 019934-001210US
CURRENT APPLICATION NUMBER: US/09/721,908
CURRENT FILING DATE: 2000-11-24
PRIOR APPLICATION NUMBER: US 60/186,626
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: human CCR10
US-09-721-908-2

Query Match 100.0%; Score 1819; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 241 VLLTVIVFIYVQLPYNIVKFCRAIDIIYSLITSCNMSKRMIDIAQVTSIALFHSCLNP 300
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DB 301 ILYVFGASFKNYVMKAKKYGSMROROSVEEPFDSGPTSTFSI 350

RESULT 3

US-09-721-341-2
Sequence 2, Application US/09721341
Patent No. 6828108
GENERAL INFORMATION:
APPLICANT: Gosling, Jennifa
APPLICANT: Dairaghi, Daniel J.
APPLICANT: Hanley, Michael
APPLICANT: Miao, Zhenhua
APPLICANT: Schall, Thomas J.
APPLICANT: Chemocentryx, Inc.
TITLE OF INVENTION: Chemokine Receptor
FILE REFERENCE: 019934-000710US
CURRENT APPLICATION NUMBER: US/09/721,341
CURRENT FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 09/686,020
PRIOR FILING DATE: 2000-10-10
PRIOR APPLICATION NUMBER: US 60/159,015
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: US 60/159,210
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 60/172,979
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 60/173,388
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/186,626
PRIOR FILING DATE: 2000-03-03
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: chemokine receptor (CXK CCR)

Query Match 100.0%; Score 1819; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 1.6e-148;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 121 INFVSGMOFLACISIDRYAVATKVPDSQGVGKPCWIIICFCVMAAILLSIPOLVFYTVND 180
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RESULT 4
US-09-721-495B-2
Sequence 2, Application US/09721495B
Patent No. 6835547
GENERAL INFORMATION:
APPLICANT: Gossling, Jennifa
APPLICANT: Dairaghi, Daniel J.
APPLICANT: Hanley, Michael
APPLICANT: Miao, Zhenhua
APPLICANT: Talbot, Dale
APPLICANT: Schell, Thomas J.
APPLICANT: Chemocentrx, Inc.
TITLE OF INVENTION: Chemokine Receptor
FILE REFERENCE: 019934-0007210US
CURRENT APPLICATION NUMBER: US/09/721,495B
PRIOR FILING DATE: 2000-11-21
PRIOR APPLICATION NUMBER: US 60/159,015
PRIOR FILING DATE: 1999-10-12
PRIOR APPLICATION NUMBER: US 60/159,210
PRIOR FILING DATE: 1999-10-13
PRIOR APPLICATION NUMBER: US 60/172,979
PRIOR FILING DATE: 1999-12-20
PRIOR APPLICATION NUMBER: US 60/173,388
PRIOR FILING DATE: 1999-12-28
PRIOR APPLICATION NUMBER: US 60/186,626
PRIOR FILING DATE: 2000-03-03
PRIOR APPLICATION NUMBER: US 09/686,019
PRIOR FILING DATE: 2000-10-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: chemokine receptor CCX CKR
US-09-721-495B-2

Query Match 100.0%; Score 1819; DB 4; Length 350;
Best Local Similarity 100.0%; Pred. No. 1,6e-148;
Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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| | | | |

Patent No. 6620615
GENERAL INFORMATION:
APPLICANT: Gould-Rothberg, Bonnie
APPLICANT: Curagen Corporation
TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR AND METHOD OF USING SAME
FILE REFERENCE: 15966-550
CURRENT APPLICATION NUMBER: US/09/556,002
CURRENT FILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: USSN 60/130,817
PRIOR FILING DATE: 1999-04-23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 350
TYPE: PRT
ORGANISM: Homo sapiens
US-09-556-002-2

Query Match 99.4%; Score 1808; DB 4; Length 350;
Best Local Similarity 99.4%; Pred. No. 1,4e-147;
Matches 348; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Db 1 MALEQNSTDYEEENMGTYDYSQYELICIKEDVREPAKVLVFLTIVFVIGLAGNS 60
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QY 61 MVAIAYKKKORTKTDVYILMLAVADLLFTLPFWANAVHGWLGKIMKITSALYT 120
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Db 61 MVAIAYKKKORTKTDVYILMLAVADLLFTLPFWANAVHGWLGKIMKITSALYT 120
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Db 121 LNFVSGMOFLACISIDRYAVATKVPQSQGVKPCWIIICFVWMAAILLSIPOLVFTYND 180
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QY 181 NARCIPIPRYLGTSMKALIQMLEICIGFVFPFLMGVCYFTARTLMKPNIKISRPLK 240
| | | | |
Db 181 NARCIPIPRYLGTSMKALIQMLEICIGFVFPFLMGVCYFTARTLMKPNIKISRPLK 240
| | | | |
QY 241 VLLTVIVIVTQLPNIVKFCRAIDIIYSLTSCMSKRMDAIQVETSIALFHSCLNP 300
| | | | |
Db 241 VLLTVIVIVTQLPNIVKFCRAIDIIYSLTSCMSKRMDAIQVETSIALFHSCLNP 300
| | | | |
QY 301 ILVFMGASFKNYVMKAKKYGSMRQROSVVEEFPDSEGPTEPTSTFSI 350
| | | | |
Db 301 ILVFMGASFKNYVMKAKKYGSMRQROSVVEEFPDSEGPTEPTSTFSI 350
| | | | |

RESULT 6
US-09-510-695-8
Sequence 8, Application US/09910695
Patent No. 6737252
GENERAL INFORMATION:
APPLICANT: Hedrick, Joseph A.
APPLICANT: Vicari, Alain P.
APPLICANT: Zlotnik, Albert
TITLE OF INVENTION: Mammalian Chemokines; Receptors;
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSER: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/910,695
FILING DATE: 20-Jul-2001

```

1  CLASSIFICATION: <Unknown>
2
3  PRIOR APPLICATION DATA:
4      APPLICATION NUMBER: 09/122,585
5      FILING DATE: 24-JUL-1998
6
7  ATTORNEY/AGENT INFORMATION:
8
9      NAME: Ching, Edwin P.
10     REGISTRATION NUMBER: 34,090
11     REFERENCE/DOCKET NUMBER: DX0755
12
13     TELECOMMUNICATION INFORMATION:
14         TELEPHONE: (650)852-9196
15         TELEFAX: (650)496-1200
16
17     INFORMATION FOR SEQ ID NO: 8:
18
19         SEQUENCE CHARACTERISTICS:
20             LENGTH: 350 amino acids
21             TYPE: amino acid
22             TOPOLOGY: linear
23
24         MOLECULE TYPE: protein
25
26         SEQUENCE DESCRIPTION: SEQ ID NO: 8:
27
28  JUS-09-910-695-8

```

Query Match	99.1%	Score 1803	DB 4	Length 350
Best Local Similarity	99.4%	Pred. No. 3.8e-147		
Matches 348	Conservative 0	Mismatches 2	Indels 0	Gaps 0
QY	1	MALBONOSTDYEEENENNGTYDYSQYELCIKEDVREFAKFLPFLVFTTIVFVIGLANS	60	
Db	1	MALEGNOSTDYEEENENNGTYDYSQYELCIKEDVREFAKFLPFLVFTTIVFVIGLANS	60	
QY	61	MVAVIYAYKKQRTKDYYIINLNAVADLLFLTPFAVNNAVHGVLCIMCKITSALYT	120	
Db	61	MVAVIYAYKKQRTKDYYIINLNAVADLLFLTPFAVNNAVHGVLCIMCKITSALYT	120	
QY	121	LNPFSGMOLFACISIDRVAAVATKVPSSGSGVKPCMIICFCVMAAIIISIPOLVYTYND	180	
Db	121	LNPFSGMOLFACISIDRVAAVATKVPSSGSGVKPCMIICFCVMAAIIISIPOLVYTYND	180	
QY	181	NARCIPIPRYLYGTSMKALIQMLEICICIFVVPFLTMGVCFYFATATLTKMPNIKISRLX	240	
Db	181	NARCIPIPRYLYGTSMKALIQMLEICICIFVVPFLTMGVCFYFATATLTKMPNIKISRLX	240	
QY	241	VLLTVVIVFIYVTOLEPYNIVKFCRAIDITYSLTSCNMSKMDIAIQVIESIALFHSCINP	300	
Db	241	VLLTVVIVFIYVTOLEPYNIVKFCRAIDITYSLTSCNMSKMDIAIQVIESIALFHSCINP	300	
QY	301	ILVYFMGSAFNKYVMKVAKKXGSMRROSOSEEPFDSGEPTEPSTESI	350	
Db	301	ILVYFMGSAFNKYVMKVAKKXGSMRROSOSEEPFDSGEPTEPSTESI	350	

```

RESULT 7
US-08-966-316-18
Sequence 18, Application US/08966316
Patent No. 5932445
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Au-Young, Janice
APPLICANT: Reddy, Roopa
APPLICANT: Murry, Lynn E.
APPLICANT: Mathur, Preete
TITLE OF INVENTION: SIGNAL PEPTIDE - CONTAINING PROTEINASES
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FaesSEQ for Windows Version 2.0

```

```

1 CURRENT APPLICATION DATA:
2 APPLICATION NUMBER: US/08/966,316
3
4 FILING DATE: Herewith
5
6 CLASSIFICATION: 435
7
8 PRIOR APPLICATION DATA:
9 APPLICATION NUMBER:
10
11 FILING DATE:
12
13 ATTORNEY/AGENT INFORMATION:
14
15 NAME: Billings, Lucy J.
16 REGISTRATION NUMBER: 36,749
17 REFERENCE/DOCKET NUMBER: PF-0424 US
18
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: 650-855-0555
21
22 TELEFAX: 650-845-4166
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25
26 TELEFAX:
27
28 INFORMATION FOR SEQ ID NO: 18:
29
30 SEQUENCE CHARACTERISTICS:
31
32 LENGTH: 350 amino acids
33
34 TYPE: amino acid
35
36 STRANDEDNESS: single
37
38 TOPOLOGY: linear
39
40 IMMEDIATE SOURCE:
41
42 LIBRARY: GenBank
43
44 CLONE: 399711
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Query Match	89.1%	Score 1620;	DB 2	Length 350;
Best Local Similarity	86.0%	Pred. No. 2e-131;		
Matches 301;	Conservative	27;	Mismatches 22;	Indels 0; Gaps 0
QY	1	MALEONOSTDYYYEENENKNGTYDYSOYELICIKEDVREAPKFLPFLPTIVFVIGLAGNS	60	
Db	1	MAVEYNGSTDYEEENENNDTHDYSQYEVLCIKERVRFAKFLPAPFTIAFIIGLAGNS	60	
QY	61	MTVAIIYAYKKKORTKTDVYIINLAVADLLFLTPFAVAVNAVHGVLGKIMKITSALYT	120	
Db	61	TVVAIIYAYKKKRRKTKTDVYIINLAVADFLFLTPFMAVAVNAVHGVLGKIMKITSALYT	120	
QY	121	LNPFSGMQLACISIDRYVAATKVPDSGQVCKPCIIIFECVMAAIIISIPOLVETVYND	180	
Db	121	VNPFSGMQLACISIDRYVAATKAPDSGQVCKPCVIFECVMAAIIISIPOLVETVYNDH	180	
QY	181	NARCIPIFPRLYLGTSMKALIQMLEICIGFVVPFLIMGVCFYFARTLKMNPINKISRLPK	240	
Db	181	KARCVPIFPRLYLGTSMKASIQILEICIGFIIPFLIMAVCFYFARTLTKMNPINKSQPLK	240	
QY	241	VLTIVVIVFVITQLPYNIYKFCRAIDITYSLITSCNMGRMDIAIQVETSIILFFHSCLP	300	
Db	241	VLFTIVVIVFVITQLPYNIYKFCQADIDITYSLITDCDMGRMDVAIQIETSIILFFHSCLP	300	
QY	301	ILVYFMGSAFKNYVMYAKKXGSMROROSVEEPFDSGPEPSTFSI	350	
Db	301	VLVYFMGSAFKNYITMKAKKXGSMRORQVNEELPFESBDATEPSTFSI	350	

RESULT 8
US-08-153-848-19
: Sequence 19, Application US/08153848
: Patent No. 5759804
: GENERAL INFORMATION:
: APPLICANT: Godlasko, Ronald
: APPLICANT: Gray, Patrick W.
: APPLICANT: Schmelkart, Vicki L.
: TITLE OF INVENTION: No. 5759804e1 Seven Transmembrane Receptors
: NUMBER OF SEQUENCES: 64
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
: ADDRESSEE: Bicknell
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: USA
: ZIP: 60606


```

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-19

```

Query Match 36.2%; Score 659; DB 1; Length 358;

Best Local Similarity 38.7%; Pred. No. 7e-49;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

```

QY 1 MLEQNSDYEEENMGTYDYSELCIKEDREPAKVPFLPFLTVFVIGLAGNS 60
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 VCLQDEVTDDYIGDNT--TVDYTLFESLCSKDVNFKAWFLPTMYSIICFVGGLNG 57
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 MVAIYAAYKKORTKTDVYILNLAVADLLFLTPMAVAHVAGWLGKIMKITSALYT 120
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 58 LVVLTYYIKRLKMTDYLNLAVADILFLTLPPMAVSAKSWFGVHFKCLIPAIYK 117
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 LNFVSGMQLACISIDRYAVATKVP--QSGVGKPCWIIICVMAAILSLIPOLVEY 176
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 118 MSFSGMILLCLISIDRYAVAIQAVSAHRRAVLLISKSCVGIMILATVISIPELVS 177
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 TVNDNA-----RCIPFPRLTSGKALIQMLEICGFVVPFLINGVCFTIARTKMKP 231
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 178 DLQRSSSEQAMRCSLITEH---VEAFITIQAVQWVIGFVPLPMSFCYLIIRTLQAR 234
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 NIKISRPALKVLTIVVFIYVITOLPYNIYKFCRAIDIIYSLTSCNSKMDIAIOVTEST 291
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 235 NERNKAIVITAVVVFIVFQLPINGVLAQTVANFNITSSITCELSKQNLAIYDVYISL 294
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 292 ALFHSGCLNLIYVFMGASPKYVMVAKKYG-----SW-----RRQRQSVBEFPDP 337
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 295 ACVRCVNPFLYAFIGVKFRNDLFKLFKDLGCLSQBLQWSSCRHRRSSMSVE----- 349
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 SECPTEPTSTFS 349
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DB 350 ----ATTTFSS 357
   : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 9

US-09-299-843A-19

Sequence 19, Application US/09299843A

Patent No. 6107475

GENERAL INFORMATION:

APPLICANT: Godiska, Ronald

APPLICANT: Gray, Patrick W.

APPLICANT: Schweikart, Vicki L.

TITLE OF INVENTION: No. 6107475el Seven Transmembrane Receptors

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESSES:

ADDRESSES: Marshall, O'Toole, Gerstein, Murray &

```

ADDRESSER: Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

```

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/299,843A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 09/088,337

FILING DATE: 01-JUN-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/153,848

FILING DATE: 17-NOV-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/977,452

FILING DATE: 17-NOV-1992

ATTORNEY/AGENT INFORMATION:

NAME: J111 E. Uhl

REGISTRATION NUMBER: 43,213

REFERENCE/DOCKET NUMBER: 27866/32059B

TELEPHONE: (312) 474-6300

TELEFAX: (312) 474-0448

TELEX:

INFORMATION FOR SEQ. ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 358 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-299-843A-19

Query Match 36.2%; Score 659; DB 3; Length 358;

Best Local Similarity 38.7%; Pred. No. 7e-49;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

```

QY 1 MLEQNSDYEEENMGTYDYSELCIKEDREPAKVPFLPFLTVFVIGLAGNS 60
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 1 VCLQDEVTDDYIGDNT--TVDYTLFESLCSKDVNFKAWFLPTMYSIICFVGGLNG 57
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 MVAIYAAYKKORTKTDVYILNLAVADLLFLTPMAVAHVAGWLGKIMKITSALYT 120
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 58 LVVLTYYIKRLKMTDYLNLAVADILFLTLPPMAVSAKSWFGVHFKCLIPAIYK 117
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 121 LNFVSGMQLACISIDRYAVATKVP--QSGVGKPCWIIICVMAAILSLIPOLVEY 176
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 118 MSFSGMILLCLISIDRYAVAIQAVSAHRRAVLLISKSCVGIMILATVISIPELVS 177
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 177 TVNDNA-----RCIPFPRLTSGKALIQMLEICGFVVPFLINGVCFTIARTKMKP 231
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 178 DLQRSSSEQAMRCSLITEH---VEAFITIQAVQWVIGFVPLPMSFCYLIIRTLQAR 234
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 232 NIKISRPALKVLTIVVFIYVITOLPYNIYKFCRAIDIIYSLTSCNSKMDIAIOVTEST 291
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 235 NERNKAIVITAVVVFIVFQLPINGVLAQTVANFNITSSITCELSKQNLAIYDVYISL 294
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 292 ALFHSGCLNLIYVFMGASPKYVMVAKKYG-----SW-----RRQRQSVBEFPDP 337
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DB 295 ACVRCVNPFLYAFIGVKFRNDLFKLFKDLGCLSQBLQWSSCRHRRSSMSVE----- 349
   : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 338 SECPTEPTSTFS 349
   : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 350 ----ATTTFSS 357
   : : : : : : : : : : : : : : : : : : : : : : : : : :

```

RESULT 10
US-09-088-337B-19
Sequence 19, Application US/09088337B
Patent No. 6348574
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: No. 6348574el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Born
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/088,337B
FILING DATE: 01-Jun-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/153,848
FILING DATE: 17-NOV-1993
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 6348574and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-088-337B-19
Query Match 36.2%; Score 659; DB 3; Length 358;
Best Local Similarity 38.7%; Pred. No. 7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 M A L E O N O S T D Y Y E E N E N G T D Y S O Y E L I C K E D V R E P A K Y F L P V L T I V V I G L A G N S 60
DB 1 V C L C O D E V T D D I G N T --- T V D Y T L F E S L C S K D V R N F K A M F L P T M Y S I I C F V G L L G N G 57
QY 61 M V V A I Y A Y Y K K O R T K T D V Y I L N L A V A D L L L F T L P F M A V N A V H G V L G K I M C K T S A L Y T 120
DB 58 L V V L Y I Y F K R L K T M D T Y L N L A V A D I L F L T L P F M A Y S A K S W F G V H F C K L I P A I Y K 117
QY 121 L N F V S G M O F L A C I S I D R Y V A V T K V P S --- Q S G V G P C W I I C F C V M A A I L S I P O L V Y 176
DB 118 M S F F S G M L L L C I S I D R Y V A I V Q A V S A H R H R A R V L I S K L S C V G I M I A T V I S I P E L L Y S 177
QY 177 T Y N D N A --- R C I P F P R Y L G T S M K A L I O M E I C I G F V V P L I N G V C F I T A R T L M K M P 231
DB 178 D I O R S S S E Q A M R S C S I T T E H --- V E A P I T T I O V A M V I G F L V P L A M S F C Y L V I I R T L L O A R 234
QY 232 N I K I S S P L K V L T V V I V T O L P Y N I V F C R A I D I I Y S L I T S C N N S K M D A I O V T E S T I 291
DB 235 N E R K A I V I T I A V V V F I V F O L P Y N G V L A Q T V A N F N I T S T C E L S K O L N I A Y D V T Y S L 294

QY 292 A L F H S C L A P I L Y E M G A S F K Y V M K V A K Y G ----- S W ----- R R O R S V E E F P P D 337
DB 295 A C V R C C V N P F L Y A F I G V F R N D L F F L F D L G L S O E O L R O W S S C H R I R S S W S V E ----- 349
QY 338 S E G P T E P T S T S 349
DB 350 --- A E T Y T T S 357
RESULT 11
PCT-US93-11153-19
Sequence 19, Application PC/TUS9311153
GENERAL INFORMATION:
APPLICANT: Godiska, Ronald
Gray, Patrick W.
Schweikart, Vicki L.
TITLE OF INVENTION: Novel Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11153
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: Noland, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 358 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-11153-19
Query Match 36.2%; Score 659; DB 5; Length 358;
Best Local Similarity 38.7%; Pred. No. 7e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
QY 1 M A L E O N O S T D Y Y E E N E N G T D Y S O Y E L I C K E D V R E P A K Y F L P V L T I V V I G L A G N S 60
DB 1 V C L C O D E V T D D I G N T --- T V D Y T L F E S L C S K D V R N F K A M F L P T M Y S I I C F V G L L G N G 57
QY 61 M V V A I Y A Y Y K K O R T K T D V Y I L N L A V A D L L L F T L P F M A V N A V H G V L G K I M C K T S A L Y T 120
DB 58 L V V L Y I Y F K R L K T M D T Y L N L A V A D I L F L T L P F M A Y S A K S W F G V H F C K L I P A I Y K 117
QY 121 L N F V S G M O F L A C I S I D R Y V A V T K V P S --- Q S G V G P C W I I C F C V M A A I L S I P O L V Y 176
DB 118 M S F F S G M L L L C I S I D R Y V A I V Q A V S A H R H R A R V L I S K L S C V G I M I A T V I S I P E L L Y S 177
QY 177 T Y N D N A --- R C I P F P R Y L G T S M K A L I O M E I C I G F V V P L I N G V C F I T A R T L M K M P 231
DB 178 D I O R S S S E Q A M R S C S I T T E H --- V E A P I T T I O V A M V I G F L V P L A M S F C Y L V I I R T L L O A R 234

```

Qy 232 NIKISRPKVLTVIVFVTVTOIPNIVKFCRAIDIIYSLTSCNMSKMDIAQVYESI 291
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 NERRKAKIVIIAAVVVVFVFOIPNPGVVALQTVANFNITTSYCELSKOLNIIYDVYSL 294
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 292 ALFHSCLNPIILVFMGASFKNYVMKRAKKYG-----SW-----RRQRQSVKEEPPD 337
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 295 ACVRCVNPPLAIFIGVKKFRNDLFKLFKDLGCLSQEQLRQWSSCRHRIIRSSMSVE----- 349
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Qy 338 SEGPTPESTTFS 349
      | : | : |
Db 350 ---AETTTTFS 357

```

```

RESULT 12
US-08-153-848-15
; Sequence 15, Application US/08153848
; Parent No. 5759804
GENERAL INFORMATION:
APPLICANT: Godleka, Ronald
APPLICANT: Gray, Patrick W.
APPLICANT: Schweikart, Vicki L.
TITLE OF INVENTION: No. 5759804el Seven Transmembrane Receptors
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: Marshail, O'Toole, Gerstein, Murray &
ADDRESSER: Bicknell
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/153,848
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/977,452
FILING DATE: 17-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: No. 5759804and, Greta E.
REGISTRATION NUMBER: 35,302
REFERENCE/DOCKET NUMBER: 31794
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 378 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-153-848-15

Query Match          36.2%; Score 659; DB 1; Length 378;
Best Local Similarity 38.7%; Pred. No. 7,4e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7

QY      1 MALBQNQSPPDYEEENHNGTYDSOVELLCIEDPREPAKVLPLPVLTIVPIYGLAGNS 60
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      21 VCLCODEVDVDDYIGDNT---TVDTYLFBESCKSDVRNFRAMPPLPVIYSIIICVGLGNG 77
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||

QY      61 MVVAIAYAYKKORTKVYIILNLAVADLLFLTPFMVAVAHVGVGKIMCKITSALYT 120
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||
Db      78 LVVLITYYIKRKJLTKMTIDTILNLNAVADIIFLLTLPLPMASVAASWVGVPFKLIPIAIYK 137
       :|::||::||::||::||::||::||::||::||::||::||::||::||::||

QY      121 LNFGSGMGFLACISIDRIYAAVTVKPS---QSGVGKPCWIICCCVMMAAILLSIPQLVFY 176

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[illegible]

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1      RESULT 13
2      US-09-299-843A-15
3      Sequence 15, Application US/09299843A
4      Patent No. 6107475
5      GENERAL INFORMATION:
6      APPLICANT: Godiska, Ronald
7      APPLICANT: Gray, Patrick W.
8      APPLICANT: Schmelkart, Vicki L.
9      TITLE OR INVENTION: No. 6107475e1 Seven Transmembrane Receptors
10     NUMBER OF SEQUENCES: 66
11     CORRESPONDENCE ADDRESS:
12     ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
13     ADDRESSEE: Borun
14     STREET: 6300 Sears Tower, 233 South Wacker Drive
15     City: Chicago
16     STATE: Illinois
17     COUNTRY: USA
18     ZIP: 60606
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Floppy disk
21     COMPUTER: IBM PC compatible
22     OPERATING SYSTEM: PC-DOS/MS-DOS
23     SOFTWARE: PatentIn Release #1.0, Version #1.25
24     CURRENT APPLICATION DATA:
25     APPLICATION NUMBER: US/09/299,843A
26     FILING DATE:
27     CLASSIFICATION: 435
28     PRIOR APPLICATION DATA:
29     APPLICATION NUMBER: US 09/088,337
30     FILING DATE: 01-JUN-1998
31     PRIOR APPLICATION DATA:
32     APPLICATION NUMBER: US 08/153,848
33     FILING DATE: 17-NOV-1993
34     PRIOR APPLICATION DATA:
35     APPLICATION NUMBER: US 07/977,452
36     FILING DATE: 17-NOV-1992
37     ATTORNEY/AGENT INFORMATION:
38     NAME: J111 E. Uhl
39     REGISTRATION NUMBER: 43,213
40     REFERENCE/DOCKET NUMBER: 27866/32059B
41     TELECOMMUNICATION INFORMATION:
42     TELEPHONE: (312) 474-6300
43     TELEFAX: (312) 474-0448
44     TELEX:
45     INFORMATION FOR SEQ ID NO: 15:
46     SEQUENCE CHARACTERISTICS:
47     LENGTH: 378 amino acids
48     TYPE: amino acid
49     TOPOLOGY: linear
50     MOLECULE TYPE: protein
51     US-09-299-843A-15

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Best Local Similarity 38.7%; Pred. No. 7, 4e-49;
Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MLEBONSQDYEEENMGNTDYSOYELICKEDVREPAKVFLLPVFLTIVFVIGLAGNS 60
DB 21 VCLCODEVTDYIDGNT--TVDYTLFESLCSKQDVNFKAMFLPIMYSIICFVGLGNG 77
QY 61 MVAIAIYAYKKORTKTDVYILNLAVADLLFLTPFWANAVHGWLGKIMCKITSALT 120
DB 78 LVVLTIVYFKRLKTMDDYLLNLAVADILFLTLFPWASAKSWFGVHFCCLIAIYK 137
QY 121 LNFVSGMOFLACISIDRYAVATKVS---QSGVGPCKWICFCVMAAILLISIPOLVY 176
DB 138 MSFSGMLLLICISIDRYAIVQAVSAHHRARVLLISKLSCVGWILATVLSIPELYS 197
QY 177 TVNDNA-----RCIPFPFYLGTSMKALIQMLEICGFVFPFLMGVCYFIARTLMKMP 231
DB 198 DIQRSSSEQAMRCSLITEN--VEAFITIQVQMWIGFLVPLPAMSFCLVIRTLQAR 254
QY 232 NIKISRPKLVLLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNSKRMDAIQVTESEI 291
DB 255 NERNKAIVIIAVVVVFIYFQLPYNGVLAQTVANFNITSTCSELKQNLAIYDVTYSL 314
QY 292 ALFHSCLNPILYVFGASFKNYVMKAKKYG-----SW-----RRORSVEEPPD 337
DB 315 ACVRCVNPFLYAFIGVFRNDLFLFKDGLGCLSGEQLRWSSCHIRRSSMSVE----- 369
QY 338 SEGPTEPSTPS 349
DB 370 ----AETTTFS 377

RESULT 14

US-09-251-545-1
; Sequence 1, Application US/09251545
; Patent No. 6153441
; GENERAL INFORMATION:
; APPLICANT: Edward R. Appelbaum
; APPLICANT: Henry M. Sarau
; APPLICANT: John R. White
; TITLE OF INVENTION: METHODS OF SCREENING FOR AGONISTS AND
; TITLE OF INVENTION: ANTAGONISTS OF THE INTERACTION BETWEEN HUMAN CCR7 RECEPTOR
; FILE REFERENCE: P50753
; CURRENT APPLICATION NUMBER: US/09/251,545
; FILING DATE: 1999-02-17
; EARLIER APPLICATION NUMBER: 60/074,883
; EARLIER FILING DATE: 1998-02-17
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Human
US-09-251-545-1

Query Match 36.2%; Score 659; DB 3; Length 378;
Best Local Similarity 38.7%; Pred. No. 7, 4e-49;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MLEBONSQDYEEENMGNTDYSOYELICKEDVREPAKVFLLPVFLTIVFVIGLAGNS 60
DB 21 VCLCODEVTDYIDGNT--TVDYTLFESLCSKQDVNFKAMFLPIMYSIICFVGLGNG 77
QY 61 MVAIAIYAYKKORTKTDVYILNLAVADLLFLTPFWANAVHGWLGKIMCKITSALT 120
DB 78 LVVLTIVYFKRLKTMDDYLLNLAVADILFLTLFPWASAKSWFGVHFCCLIAIYK 137
QY 121 LNFVSGMOFLACISIDRYAVATKVS---QSGVGPCKWICFCVMAAILLISIPOLVY 176
DB 138 MSFSGMLLLICISIDRYAIVQAVSAHHRARVLLISKLSCVGWILATVLSIPELYS 197
QY 177 TVNDNA-----RCIPFPFYLGTSMKALIQMLEICGFVFPFLMGVCYFIARTLMKMP 231

DB 198 DIQRSSSEQAMRCSLITEN--VEAFITIQVQMWIGFLVPLPAMSFCLVIRTLQAR 254
QY 232 NIKISRPKLVLLTVIVFIVTQLPYNIYKFCRAIDIIYSLITSCNSKRMDAIQVTESEI 291
DB 255 NERNKAIVIIAVVVVFIYFQLPYNGVLAQTVANFNITSTCSELKQNLAIYDVTYSL 314
QY 292 ALFHSCLNPILYVFGASFKNYVMKAKKYG-----SW-----RRORSVEEPPD 337
DB 315 ACVRCVNPFLYAFIGVFRNDLFLFKDGLGCLSGEQLRWSSCHIRRSSMSVE----- 369
QY 338 SEGPTEPSTPS 349
DB 370 ----AETTTFS 377

RESULT 15

US-09-088-337B-15
; Sequence 15, Application US/09088337B
; Patent No. 6348574
; GENERAL INFORMATION:
; APPLICANT: Godiska, Ronald
; Gray, Patrick W.
; SchweiKart, Vicki L.
; TITLE OF INVENTION: No. 6348574e1 Seven Transmembrane Receptors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/088,337B
; FILING DATE: 01-Jun-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/153,848
; FILING DATE: 17-NOV-1993
; APPLICATION NUMBER: US 07/977,452
; FILING DATE: 17-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: No. 6348574and, Greta E.
; REGISTRATION NUMBER: 35,302
; REFERENCE/DOCKET NUMBER: 31794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 474-6300
; TELEFAX: (312) 474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 378 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-088-337B-15

Query Match 36.2%; Score 659; DB 3; Length 378;
Best Local Similarity 38.7%; Pred. No. 7, 4e-49;

Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;

QY 1 MLEBONSQDYEEENMGNTDYSOYELICKEDVREPAKVFLLPVFLTIVFVIGLAGNS 60
DB 21 VCLCODEVTDYIDGNT--TVDYTLFESLCSKQDVNFKAMFLPIMYSIICFVGLGNG 77

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 2, 2005, 04:13:51 ; Search time 19 Seconds

(without alignments)
1772.414 Million cell updates/sec

Title: US-09-721-341-2

Perfect score: 1819
Sequence: 1 MALEONOSTDYEEENENMG.....VEEFPDSGPTPEPTSTFSI 350

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1620	89.1	350	2 JN0621	G protein-coupled
2	659	36.2	378	2 B55735	Lymphocyte-specific
3	650	35.7	378	2 A55735	G protein-coupled
4	643	35.3	378	2 A45680	G protein-coupled
5	583	33.1	369	2 JCS068	G protein-coupled
6	537.5	29.5	360	2 A57160	chemokine (C-C) re
7	534.5	29.4	360	2 A53611	interleukin-8 rece
8	524	28.8	354	2 I58186	probable G protein
9	522.5	28.7	350	2 JCS044	orphan G protein-c
10	522.5	28.7	360	2 JCS044	chemokine (C-C) re
11	518.5	26.5	354	2 B55733	G protein-coupled
12	511	28.1	358	2 A53752	interleukin-8 rece
13	501.5	27.6	355	2 J01231	interleukin-8 rece
14	500.5	27.5	352	2 A45747	neuropeptide Y/pep
15	499.5	27.5	353	2 S28787	neuropeptide Y/pep
16	493.5	27.0	352	2 G00048	fusin (LESTRA) - c
17	492	27.0	360	2 JCS243	chemokine (C-C) re
18	489.5	26.9	350	2 A39445	interleukin-8 rece
19	486	26.7	355	2 JCS067	G protein-coupled
20	485	26.7	355	2 I49339	macrophage inflam
21	484.5	26.6	352	2 A43113	chemokine (C-C) re
22	483.5	26.6	359	2 A48921	interleukin-8 rece
23	482	26.5	374	2 I38450	chemokine (C-C) re
24	479.5	26.4	359	2 I49341	MIP-1 alpha recept
25	476.5	26.2	367	2 JCS049	interferon-inducib
26	474	26.1	355	2 A45177	chemokine (C-C) re
27	471	25.9	356	2 S42096	interleukin-8 rece
28	470	25.8	383	2 S55594	G protein-coupled
29	461.5	25.4	355	2 G02436	chemokine (C-C) re

30	455.5	25.0	359	2 S44425	angiotensin II rec
31	452.5	24.9	359	2 JCS104	angiotensin II rec
32	452.5	24.9	359	2 JCS134	angiotensin II rec
33	450	24.7	359	2 S15403	angiotensin II rec
34	450	24.7	374	2 S32785	G protein-coupled
35	446.5	24.5	359	2 A48857	angiotensin II rec
36	445.5	24.5	356	2 I49340	MIP-1 alpha recept
37	442.5	24.3	372	2 S26667	G protein-coupled
38	442.5	24.3	374	2 S42628	G protein-coupled
39	441	24.2	362	2 JN0694	angiotensin II rec
40	439	24.1	359	2 A42656	angiotensin II rec
41	438.5	24.1	359	2 JH0621	angiotensin II rec
42	438.5	24.1	362	2 A39714	angiotensin II rec
43	437.5	24.1	327	2 S56162	G protein-coupled
44	434	23.9	359	2 J05162	MDC15 protein - h
45	428.5	23.6	359	2 I39418	angiotensin II rec

ALIGNMENTS

RESULT 1

JN0621
G protein-coupled receptor type B - bovine
C:Species: Bos primigenius taurus (cattle)
C>Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

C:Accession: JN0621
R:Matsumoto, I.; Mori, T.; Aoki, J.; Sato, T.; Kurihara, K.
Biochem. Biophys. Res. Commun. 194, 504-511, 1993

A:Title: Identification of novel members of G-protein coupled receptor superfamily expr
A:Reference number: JN0621; MUID:93326166; PMID:8392843

A:Accession: JN0621

A:Molecule type: mRNA

A:Residues: 1-350 <MAT>

A:Cross-references: UNIPROT:P35350; GB:S63848; NID:G399710; PIDN:AAB27547.1; PID:G399711

A:Experimental source: tongue taste papillae

C:Comment: This protein is involved in modulating taste sensitivity or regeneration of t

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; glycoprotein; receptor; transmembrane protein

F:42-66/Domain: transmembrane #status predicted <TM1>

F:80-99/Domain: transmembrane #status predicted <TM2>

F:114-135/Domain: transmembrane #status predicted <TM3>

F:154-175/Domain: transmembrane #status predicted <TM4>

F:200-222/Domain: transmembrane #status predicted <TM5>

F:242-265/Domain: transmembrane #status predicted <TM6>

F:284-306/Domain: transmembrane #status predicted <TM7>

F:6,19/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 89.1% Score 1620; DB 2; Length 350;

Best Local Similarity 86.0% Pred. No. 1,1e-130; Mismatches 22; Indels 0; Gaps 0;

Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY	1	MALEONOSTDYEEENENMGTYDSQYELICIKEDVREBAKFLPVFLTIVEVIGLAGNS	60
DB	1	MAVEYNOSTDYEEENENMDTHDSQYEVICKEERKAKFLPFAFTIATIGLAGNS	60
QY	61	MVAAYIAYKKKORTTDTYIIMLAVADLLFTLPFAVNAVHGVNLGIMCKITSALYT	120
DB	61	TVAAYIAYKKKRTITDYIIMLAVADLLFTLPFAVNAVHGVNLGIMCKITSALYT	120
QY	121	LNFAVGMOFLACISIDRYAVAVTKVPSQSGVKPCWICGCVMAAILISIPOLVFYTVND	180
DB	121	VAFVSGMOFLACISIDRYAVAVTKASQSGVGRPCWICGCVMAAILISIPOLVFYTVNH	180
QY	181	NARCIPIPRVYGTSMKALLQMLEICIGFVFLIMGVCFITARTLMKMPIKISRPX	240
DB	181	KARCVPIPRVYHGTSMKASIQLEICIGFIIPFLIMAVCYFITAKTLIMPKIKSQPX	240
QY	241	VLTIVYVPIYIQTLPYNYIVKPRADIIYSLTSCMSRMKMAIQVESIALFFISCLNP	300
DB	241	VLETVVYVPIYIQTLPYNYIVKPCQADIIYSLTSDMSRMDVAIQIESIALFFISCLNP	300
QY	301	ILYVFMGASFKNYVMKAKYGSMPRQROSVEEFPDSGPTPEPTSTFSI	350


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Db      21 VCLCODEVTDDYIGDNT---TVDYTLFESLCKKDVNFKAMFLPINTSYICFVGLLNG 77
Qy      61 MVAIATAYKKQRTKTDVYILNLAADLLFLTPFAVANAAGVWLGMCKITSAIYT 120
Db      78 LVVLTITFERLKTMDYILNLAADILFLTLTPFAVSAASWGVFCKLITAIYK 137
Qy      121 LNFVSGMQLACISIDRYAVATKVPQSOGVKPCWII--CFCYMMA--AIIISIPOLVF 16
Db      138 MSFSGMULLCISIDRYAIVAVASAHRRARVALLSKSCVSAIATVLSIPELYS 197
Qy      177 TVNDA-----RCIPFPRLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKP 231
Db      198 DLQSSSEQAMRCSLITEH---VEAFITIQAGVIGFVLPLAMSPCYVIIITLLQAR 254
Qy      232 NIKISPLKVLTVVVFYITQLPYNIYKFCRAIDIIYSITSCNMSKMDIAIQTESI 291
Db      255 NEERNKAIVIAVVFVIFQLPYNGVLAQTVAFNITSTCELSKQINIVDYATSL 314
Qy      292 ALPHSCLNPLILYFMGASPKNYVMKAKKYG-----SM-----RRQROSVPEPPD 337
Db      315 ACRCVNPFLYAFIVKFRNDIFKLKDLGCLSQEQLROMSSCRHRRSMSEV----- 369
Qy      338 SEGPTEPTSTFS 349
Db      370 ---AETTTFS 377

RESULT 5
G protein-coupled receptor CKR-L3 - human
C/Species: Homo sapiens (man)
C/Date: 31-Jan-1997 #sequence_revision 31-Jan-1997 #text_change 21-Jul-2000
C/Accession: JCS068
R/Label: A.; Varona, R.; Galtier, J.; Lind, P.; Marquez, G.
Biochem. Biophys. Res. Commun. 227, 846-853, 1996
A/Title: Molecular cloning and RNA expression of two new human chemokine receptor-like G
A/Reference number: JCS067, PMID:97040707, PMID:8886020
A/Accession: JCS068
A/Molecule type: DNA
A/Residues: 1-369 <TAB>
A/Cross-references: EMBL:279784; NID:G1668737; PIDN:CA02144.1; PID:G1668738
C/Comment: This protein belongs to the family of alpha chemokine receptors.
C/Genetics:
A/Genes: GDB:CMKBR6; STRL22; GPR29; CCR6; CKR-L3; GPR-CY4
A/Map position: 6q27-6q27
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; transmembrane protein
F/42-68/Domain: transmembrane #status predicted <TM1>
F/79-99/Domain: transmembrane #status predicted <TM2>
F/115-136/Domain: transmembrane #status predicted <TM3>
F/160-180/Domain: transmembrane #status predicted <TM4>
F/212-233/Domain: transmembrane #status predicted <TM5>
F/250-271/Domain: transmembrane #status predicted <TM6>
F/292-315/Domain: transmembrane #status predicted <TM7>

Query Match      32.1%; Score 583; DB 2; Length 369;
Best Local Similarity 36.1%; Pred. No. 3.3e-42;
Matches 121; Conservative 68; Mismatches 120; Indels 26; Gaps 7;

Qy      8 STDYEEENMGTYDYSQVELICIKEDVREPAKFLPVFLTVFVIGLAGNSMVAIYA 67
Db      18 NTSYVDSBM-----LCSIOEYQVFSRLFPVIVSLICVFGILGNLIVITPA 67
Qy      68 YXKQRTKTDVYILNLAADLLFLTPFAV-NAVHGVLGKIMCKITSAIYTLNFSVG 126
Db      68 FYKASMTDVLILNLAADILFLTLTPFAVSHATGAVFVSNAATGLKGIYAINENCG 127
Qy      127 MQLACISIDRYAVATKVP-----QSGVKPCWIIICFCYMAAIIISIPOLVF---YTVN 179
Db      128 MLLTITSDIRYIAIVQATKSPRLRSITLPRSKITCLVWGLSVIISSTFVFNOKNTO 187
Qy      180 DNARCIPIPRYLGTG-----MKALIQLMEICIGFVVPFLIMGVCFITARTLMKMPNIKI 235

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Db      188 GSDVC---EPKQTVSEPIRKWLKLMGLTELPFFPIPLMFICFYFIKTVLQAQNSKR 244
Qy      236 SRPLKLLVTVVVFYITQLPYNIYKFCRAIDIIYSITSCNMSKMDIAIQTESIATLR 295
Db      245 HKAIRVIAVVFVFLCOIPHNVLVLTAAV-LGKNRSCQSEKLIQYTKTVLEVALFHL 303
Qy      296 SCINPLIYVFMGASPKNYVMKAKKYGSWRROROS 330
Db      304 CCLNPLVIAVFIQGFRRNFKLTKLMDLVRRKTKS 338

RESULT 6
chemokine (C-C) receptor 4 - human
N/Alternate names: C-C CKR-4
C/Species: Homo sapiens (man)
C/Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: A57160
R/Power: C.A.; Meyer, A.; Nemeth, K.; Bacon, K.B.; Hoogewerf, A.J.; Proudfoot, A.E.I.;
J. Biol. Chem. 270, 19495-19500, 1995
A/Title: Molecular cloning and functional expression of a novel CC chemokine receptor c
A/Reference number: A57160; PMID:95370289; PMID:7642634
A/Accession: A57160
A/Status: Preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-360 <POM>
A/Cross-references: UNIPROT:P51679; GB:X85740; NID:G1370103; PIDN:CA059743.1; PID:G9714
A/Note: source clone KS-5
C/Genetics:
A/Genes: GDB:CMKBR4
A/Cross-references: GDB:677463
A/Map position: 3p21-3p21
C/Superfamily: vertebrate rhodopsin
C/Keywords: G protein-coupled receptor; glycoprotein; phosphoprotein; transmembrane pro
F/40-65/Domain: transmembrane #status predicted <TM1>
F/76-97/Domain: transmembrane #status predicted <TM2>
F/112-133/Domain: transmembrane #status predicted <TM3>
F/151-175/Domain: transmembrane #status predicted <TM4>
F/208-226/Domain: transmembrane #status predicted <TM5>
F/243-264/Domain: transmembrane #status predicted <TM6>
F/291-308/Domain: transmembrane #status predicted <TM7>
F/29-276.110-187/Disulfide bonds: #status predicted
F/72.350/Binding site: phosphate (Ser) (covalent) (by casein kinase II) #status predict
F/143/Binding site: phosphate (Ser) (covalent) (by protein kinase C) #status predicted
F/183.194/Binding site: carbonylrate (Asn) (covalent) #status predicted
F/321/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted

Query Match      29.5%; Score 537.5; DB 2; Length 360;
Best Local Similarity 35.8%; Pred. No. 2.5e-38;
Matches 115; Conservative 63; Mismatches 124; Indels 19; Gaps 6;

Qy      10 DYYEENENMGTYDYSQVELICIKEDVREPAKFLPVFLTVFVIGLAGNSMVAIYAY 69
Db      8 DTLDESIYSNVYLVSIEPKCTKKGIKAFGLFLPLVLSLVFVFGILGNSVVVLVLFKY 67
Qy      70 KKQRTKTDVYILNLAADLLFLTPFAVANAAGVWLGMCKITSAIYTLNFSVGMP 129
Db      68 KRLRSMTDVLILNLAIDLLFVFSLPFGWYADQVFGIGCKMISMVYLGVSGIFP 127
Qy      130 LACISIDRYAVATKV-----PSQSGVKPCWIIICFCYMAAIIISIPOLVF---YTVN 179
Db      128 VMLMSIDRLIAYHAVFSRLARTITGV-----ITSLATRSVAVFASLGEFLSTCYTER 182
Qy      180 DNARCIPIPRYLGTSMKALIQMLEI-CIGFVVPFLIMGVCFITARTLMKMPNIKI SRP 238
Db      183 NHTYCKTKTKS--LNSTTKVWLSLEINILGLVPLIGIMFCYSMIIRTLQHCNKKKNA 240
Qy      239 LKVLTVVVFYITQLPYNIYKFCRAIDIIYSITSCNMSKMDIAIQTESIATLHSC 298
Db      241 VKMIFAVVVLVFLGFWTPYNIIVFLETL-VELEVLQDCTFERYLDVAIQATETLAFVHCL 299
Qy      299 NPILYVFMGASPKNYVMKAK 319

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Db 300 NPIYFFLGEKFRKYLQFLK 320

RESULT 7

Interleukin-8 receptor type B - human

C:Species: Homo sapiens (man)

C:Date: 07-Oct-1994 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004

C:Accession: I37898; I38712; A53611; A39446

R:Ahuja, S.K.; Shetty, A.; Tiffany, H.L.; Murphy, P.M.

J. Biol. Chem. 269, 26381-26389, 1994

A:Title: Comparison of the genomic organization and promoter function for human interleukin-8

A:Reference number: I37898; MUID:95014476; PMID:7929358

A:Accession: I37898

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-360 <RES>

A:Cross-references: UNIPROT:P25025; EMBL:U11869; NID:G511801; PIDN:AAB60656.1; PID:G5118

A:Accession: I38712

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-15 <RES>

A:Cross-references: EMBL:U11872; NID:G511808; PIDN:AAA64380.1; PID:G511809; EMBL:U11873; I1876; NID:G511816; PID:G511817; EMBL:U11877; NID:G511818; PID:G511819; EMBL:U11878; NID

R:Spengler, H.; Lloyd, A.R.; Laurens, L.L.; Bonner, T.I.; Keltvin, D.J.

J. Biol. Chem. 269, 11065-11072, 1994

A:Title: Structure, genomic organization, and expression of the human interleukin-8 receptor

A:Reference number: A53611; MUID:94209273; PMID:7512557

A:Accession: A53611

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 6-360 <SPR>

A:Cross-references: GB:M99412; GB:IL19593

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 6-360 <MUR>

A:Cross-references: GB:M73969

C:Comment: This receptor, unlike IL8RA, binds several peptides besides interleukin-8, in

C:Genetics:

A:Gene: IL8RA

A:Cross-references: GDB:I27868; OMIM:146928

A:Map position: 2q35-2q35

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match

Best Local Similarity 33.2%; Score 534.5; DB 2; Length 360;

Matches 120; Conservative 75; Mismatches 141; Indels 25; Gaps 8;

3 LEQNGSTDYEEENMGTYDSQYELI-----CIKEDVREFAKFLPVFLTVFVYIGLA 57

6 MESDSFEDFPKGGDLNYSSTLPFLDAAACPEBSL-EINKYFVILYALVFLSL 64

58 GNSMVAIYAYKKQRTKTDVYLNLAVADLLFLTPMAVNAVHGVLGKIMCKITSA 117

65 GNSLVMVLVILYRSGSVTDVYLNLADLLPALTLPIWAASKVGMIGFTFLCKVSL 124

118 LYLTVFVSGMQLACTSIDRYVAV---TKVPSQSGVCKPCWIIICFCVMAAILLSIPQV 174

125 LKEVNYISGLLIACISVDRIYLAIVHATRTLTGRY-LVKFCLSLWGLSLILALPVL 182

175 F---TYVNDNARCIPIFPFVTLG---TSMKALIQMLEICIGFVFPFLIMGVCFITARTL 227

183 FRTVYSSNVSPACY---EDMGNNTANRWMRLRIIPQSGFIVPLILMFCGFTLRTL 238

228 MKKPNIKISRPALVLTIVIVITVTLQPNIVKFCRAIDIIYSLITSCNMSKMDIAIQ 287

Db 239 FRAHNGQKRAMRVIAVAVLLFCMLPYNVLADLTMRTOVIOETCERRNHIDBALDA 298

288 TESIALFHSCLNPIIYVFWGASFKNYVMKAKKYSWRQ---ROSVSEFPDSEGPTEP 344

299 TELIGLHSCLNPLIYAFIIGQKFRHGLKILAIHGLISKDSLPKOSRPFVSSSGHTST 358

Qy 345 T 345

Db 359 T 359

RESULT 8

I58186

probable G protein-coupled receptor - rat

C:Species: Rattus norvegicus (Norway rat)

C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004

C:Accession: I58186

R:Harrison, J.K.; Barber, C.M.; Lynch, K.R.

Neurosci. Lett. 169, 85-89, 1994

A:Title: CDNA cloning of a G-protein-coupled receptor expressed in rat spinal cord and b

A:Reference number: I58186; MUID:94323113; PMID:8047298

A:Accession: I58186

A:Status: preliminary; translated from GB/EMBL/DBD

A:Molecule type: mRNA

A:Residues: 1-354 <RES>

A:Cross-references: UNIPROT:P35411; EMBL:U04808; NID:G2558635; PIDN:AAB87093.1; PID:G439

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor

Query Match

Best Local Similarity 36.9%; Score 524; DB 2; Length 354;

Matches 113; Conservative 51; Mismatches 128; Indels 14; Gaps 4;

22 YDYSQYELCIKEDVREFAKFLPVFLTVFVYIGLAGNMAVAYKKQRTKTDVYL 81

13 FEYDSSAEACVYGDIAFETIFLSIFSVLFTFGLVGNLVLALTNKSKSIDIYLL 72

82 NLAVADLLFLTPMAVNAVHGVLGKIMCKITSAIYTLNFSQMQLACTSIDRYAV 141

73 NLALSDLLFVALTLFPFTHYLISHBGLHNMCKLTATFAFFIGFGIFFTVISIDRYLAI 132

142 TKVPS-----QSGVCKPCWIIICFCVMAAILLSIPQVFTVNDNARCIPIFPYIGT 194

133 VLAASNNRRTVQHG-----TISLGVMAAAILVASPOPMFTFRKDN-BCLDYPREVLOE 186

195 SMKALIQMLEICIGFVFPFLIMGVCFITARTIMKPNIKISRPALKVLTIVIVITVTLQ 254

187 IMPVLNRSVNIIGFVLPFLIMSFCTFRIVRTLFSCKNRKARAIPLILVAVVFPFLWT 246

255 PNIIVKFCRAIDIIYSLITSCNMSKMDIAIOVTESIALFHSCLNPLIYVFGASFKNYV 314

247 PNIIVFLETLK-FYVFPSPCGMKDLRWALSVTEVAVASHCCLNPLIYAFAGEKFRYTL 305

Qy 315 MKVAKK 320

Db 306 RHLVYK 311

RESULT 9

JC4304

Orphan G protein-coupled receptor - human

N:Alternate names: V28 protein

C:Species: Homo sapiens (man)

C:Date: 16-Nov-1995 #sequence_revision 08-Feb-1996 #text_change 09-Jul-2004

C:Accession: JC4304

R:Raport, C.J.; Schweickart, V.L.; Eddy Jr., R.L.; Shows, T.B.; Gray, P.W.

Gene 163, 295-299, 1995

A:Title: The Orphan G-protein-coupled receptor-encoding gene V28 is closely related to

A:Reference number: JC4304; MUID:96011651; PMID:7590284

A:Accession: JC4304

A:Molecule type: mRNA

A:Residues: 1-355 <RAP>

A:Cross-references: UNIPROT:P49238; GB:U20350; NID:G665580; PIDN:AAA91783.1; PID:G665581

Db 303 AFLGPFRODLRLRLRGSSPSGPOPRRCRCPPRRPLS-----SCSAPETETSL 350

RESULT 12

A53752

Interleukin-8 receptor (clone 5B1a) - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #ext_change 09-Jul-2004

C:Accession: A53752

R:Prado, G.N.; Thomas, K.M.; Suzuki, H.; Larosa, G.J.; Wilkinson, N.; Folco, E.; Navarro

J. Biol. Chem. 269, 12391-12394, 1994

A:Title: Molecular characterization of a novel rabbit interleukin-8 receptor isoform.

A:Reference number: A53752; MUID:94230294; PMID:8175642

A:Accession: A53752

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-358 <P>

A:Cross-references: UNIPROT:P35344; GB:U24445; NID:g437661; PIDN:AAA31378.1; PID:g437662

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 28.1%; Score 511; DB 2; Length 358;
Best Local Similarity 32.3%; Pred. No. 4, 5e-36;
Matches 116; Conservative 72; Mismatches 139; Indels 32; Gaps 8;

10 DYVEENENMGTVDSQVELI-----CIKEDVEFAKVPVPLTVFVIGLA 57

8 NYSYE--DFPG--DEFNYSYSTDLPTLLDSAPCESLETNSYVLLIYI-LVFLSL 62

58 GNSMVVAIYAYKKQRTQDVITLAVADLLFLPLPFAVAVAHGVGLKIMCKITSA 117

63 GNSLWMLVILYRSSTCSVDVLLNLAIDLFLFATLPIMAASKVHGMFEGPLCKVSL 122

118 LVTLPVSGMQLACISIDRYAV-----TKVPSQSGVCKPCMIICFCVMAAILISIQ 172

123 VEVNMFYSGLILACISVRYALVHATRTMTQKRLVK---PILSMGVSLISLPI 178

173 LVFVYVNDNARCIPIPRYIGTS---MKALIQMLEICGFVVPFLMGVCYFTARTLTK 229

179 LIFRNAIFPPNSPVCYEDMGSTAKRNVRLPOTPFILPLVLMFCYVETLTLTQ 238

230 MNKISRLPKVLLTVIVIVITQDPYNTVYKFCRAIDIIYSLTSCNMSKMDIAIQVTE 289

233 AHMGQKRRARVFAVVLFLFCWLPYNNVLLDTLMRTHVIOETCERRNDIDRADATE 298

290 STALFSCNPLIYVYMGASFKYVWKVKKYGSWRQ---RQSVDEPPDSGPRTEPT 345

299 ILGFLHSCNPLIYAFYIGQKFRYGLKILIAHGLISKEFLAKESRPSFVASSSGNTSTT 357

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

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QY

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QY

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QY

Db

QY

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QY

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QY

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QY

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QY

Db

QY

Db

A:Experimental source: neutrophils

A>Note: sequence extracted from NCBI backbone (NCBIN:81526, NCBI:81530)

C:Superfamily: vertebrate rhodopsin

C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match 27.6%; Score 501.5; DB 2; Length 355;
Best Local Similarity 33.1%; Pred. No. 2, 9e-35;
Matches 107; Conservative 70; Mismatches 127; Indels 19; Gaps 6;

12 YVEENENMGTVDSQVELI-----YDSQVELCIKEDVEFAKVPVPLTVFVIGLAGNSMVVAI 65

14 WEDSEFANATGMPPEKYS--PCLVITQTLKVVV--VYALVFLSLGNSLVMV 68

66 YAYVKQRTQDVITLAVADLLFLPLPFAVAVAHGVGLKIMCKITSAIYTLNFS 125

69 ILYSRNSVTDVITLAVADLLFLPLPFAVAVAHGVGLKIMCKITSAIYTLNFS 128

126 GQVFLACISIDRYAV-----TKVPSQSGVCKPCMIICFCVMAAILISIQVLYTYNDNA 182

129 GILLACISVDRYALVHATRTLTQK--RHLVKFICLGMALSLISLPLFLRQVFSFN 186

183 RCIPFPRYIG--TSMKALIQMLEICGFVVPFLMGVCYFTARTLTKMKNISRL 239

187 NSSPVCYEDLGNITAKRWVRLIHPHTFGLPLVLMFCYFTARTLTFQAMGQKRRM 246

240 KVLTVIVITQDPYNTVYKFCRAIDIIYSLTSCNMSKMDIAIQVTEIAPHSCLN 299

247 RVIPAVVILFLCWLPPYVLLADTLMRTHVIOETCERRNDIDRADATEILGFLHSCIN 306

300 PLIYVFMGASFKYVWKVKKYGSWRQ---RQSVDEPPDSGPRTEPT 345

307 PLIYAFIGQNFNGFLKMLAARG 329

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

Db

QY

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QY

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QY

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QY

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QY

Db

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OM protein - protein search, using sw model

Run on: March 2, 2005, 04:14:37 ; Search time 66 seconds
(without alignments)
2715.571 Million cell updates/sec

Title: US-09-721-341-2

Perfect score: 1819

Sequence: 1 MALEGNQSDYEEENMG.....VEFPDSDGPTPTSTFSI 350

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1819	100.0	350	1	CKRB_HUMAN
2	1620	89.1	350	1	CKRB_BOVIN
3	1526	87.7	350	2	Q924T3
4	1594	87.6	350	2	Q8C0M1
5	1593	87.6	350	2	Q8QZM9
6	1070	58.8	356	2	Q63ZL5
7	912	50.1	221	2	Q9SEK1
8	663	36.4	369	2	Q6Y747
9	659	36.2	378	1	CKR7_HUMAN
10	657	36.1	357	2	Q6Y746
11	657	36.1	378	2	Q8H2R6
12	650	35.7	378	1	CKR7_MOUSE
13	649	35.7	358	2	Q6G958
14	648	35.6	378	2	Q8C8S2
15	646	35.5	378	2	Q6U2D6
16	645.5	35.5	380	2	Q861S1
17	643	35.3	369	2	Q9UQ06
18	643	35.3	369	2	Q8CH33
19	639	35.1	369	1	CKR9_MOUSE
20	637	35.0	357	1	CKR9_HUMAN
21	629.5	34.6	382	2	Q707H3
22	612.5	33.7	325	2	Q677Y8
23	611	33.6	367	2	Q9R1V0
24	608.5	33.5	369	2	Q76L89
25	605	33.3	367	1	CKR6_MOUSE
26	598	32.9	341	2	Q6Y744
27	586.5	32.2	368	2	Q42444
28	583	32.1	374	1	CKR6_HUMAN
29	583	32.1	374	2	Q8H2R7
30	581	31.9	342	1	CKR6_CERAE
31	578	31.8	343	2	Q9N0Z0

32	571	31.4	343	1	CKR6_MACMU	Q9XC45 macaca mula
33	569	31.3	342	1	CKR6_MACNE	Q19024 macaca neme
34	566.5	31.1	351	2	Q9S0L6	Q9S0L6 mus musculus
35	566	31.1	343	1	CKR6_MACFA	Q9B066 macaca faec
36	561.5	30.9	351	2	Q9SRH5	Q9SRH5 mus musculus
37	560	30.8	333	2	Q678F3	Q678F3 lymphocysti
38	560	30.8	342	1	CKR6_HUMAN	Q00574 homo sapien
39	560	30.8	342	2	Q9H0A5	Q9H0A5 homo sapien
40	559	30.7	342	1	CKR6_PANTR	Q9TV16 pan troglod
41	544	29.9	358	2	Q9PUA0	Q9PUA0 acipenser t
42	537.5	29.5	360	1	CKR4_HUMAN	P51679 homo sapien
43	535.5	29.4	355	2	Q8H2N7	Q8H2N7 gorilla gor
44	534.5	29.4	355	2	Q8H2N6	Q8H2N6 pongo pygma
45	534.5	29.4	355	2	Q8H2N8	Q8H2N8 pan troglod

ALIGNMENTS

RESULT 1

ID	CKRB_HUMAN	STANDARD	PRT	350 AA.
AC	Q9NPB9			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	C-C chemokine receptor type 11 (C-C CKR-11) (CCR-11)			
DE	(Chemokine receptor-like 1) (CCR1) (CCX CKR).			
GN	Name=CCR1; Synonyms=CCBP2, CCR11, VSHK1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20200450; PubMed=10734104; DOI=10.1074/jbc.275.13.9550;			
RA	Schweickart V.L., Epp A., Raport C.J., Gray P.W.;			
RT	"CCR1 is a functional receptor for the monocyte chemoattractant protein family of chemokines."			
RL	J. Biol. Chem. 275:9550-9556 (2000).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20171478; PubMed=10706668;			
RA	Goelings J., Dairaghi D.J., Wang Y., Hanley M., Talbot D., Miao Z.,			
RT	Schall T.J.;			
RL	"Identification of a novel chemokine receptor that binds dendritic cell- and T cell-active chemokines including ELC, SLC, and TECK."			
RL	J. Immunol. 164:2851-2856 (2000).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=20231748; PubMed=10767544; DOI=10.1016/S0378-1119(00)00076-7;			
RA	Khoja H., Wang G., Ng C.-T.L., Tucker J., Brown T., Shyamala V.;			
RT	"Cloning of CCR1, an orphan seven transmembrane receptor related to chemokine receptors, expressed abundantly in the heart."			
RL	Gene 246:229-238 (2000).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RA	Kopatz S.A., Aronstam R.S., Sharma S.V.;			
RT	"cDNA clones of human proteins involved in signal transduction regulated by the G-protein coupled receptor (www.cdn.org).";			
RL	Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.			
CC	-1- FUNCTION: Receptor for SCY2/MCP1, SCY2/MCP2, SCY13/MCP4.			
CC	SCY19/MIP3/ELC, SCY21/SIC and SCY25/TECK.			
CC	-1- SUBCELLULAR LOCATION: Integral membrane protein.			
CC	-1- TISSUE SPECIFICITY: Predominantly expressed in heart. Lower expression in lung, pancreas, spleen, small intestine and fetal tissues.			
CC	-1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way			

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CC EMBL; AF193507; AAF61299.1; -;
 CC EMBL; AF233281; AAF44751.1; -;
 CC EMBL; AF110640; AAF59827.1; -;
 CC EMBL; AY221094; AAF05972.1; -;
 CC Genbank; HGNC:1611; CCRL1.
 DR GO; GO:0005887; C.integral to plasma membrane; TAS.
 DR GO; GO:0004950; P.chemokine receptor activity; TAS.
 DR GO; GO:0006935; P.chemokine; TAS.
 DR GO; GO:0007186; P.G-protein coupled receptor protein signalin. . .; TAS.
 DR GO; GO:0006955; P.immune response; TAS.
 DR InterPro; IPR005383; CC 11 receptor.
 DR InterPro; IPR000355; Chk1kinase receptor.
 DR InterPro; IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1, 1.
 DR PRINTS; PRO1558; CHEMOKINER11.
 DR PRINTS; PRO0237; GPCR_RHODOPSN.
 DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Glycoprotein; Transmembrane.
 FT DOMAIN 1 42
 FT TRANSMEM 43 63
 FT TRANSMEM 64 87
 FT TRANSMEM 88 108
 FT TRANSMEM 109 113
 FT TRANSMEM 114 134
 FT TRANSMEM 135 154
 FT TRANSMEM 155 175
 FT TRANSMEM 176 201
 FT TRANSMEM 202 222
 FT TRANSMEM 223 240
 FT TRANSMEM 241 261
 FT TRANSMEM 262 289
 FT TRANSMEM 290 310
 FT TRANSMEM 311 350
 FT CARBOHYD 6 6
 FT CARBOHYD 19 19
 FT DISULFID 112 184
 FT SEQUENCE 350 AA; 39913 MW; 8E26049D25757C8 CRC64;

Query Match 100.0%; Score 1819; DB 1; Length 350;
 Best Local Similarity 100.0%; Pred. No. 2; Se-103;
 Matches 350; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALEONQSTDYEEENENNGTGYDYSQYELICIKEDVREFAKVPFLPVFLTIVFVIGLAGNS 60
 DB 1 MALEONQSTDYEEENENNGTGYDYSQYELICIKEDVREFAKVPFLPVFLTIVFVIGLAGNS 60
 QY 61 MVAIAIYVKKKORTKTDVYTLINAVADLLFTLPWANAANAVGWLGIKMKCTITALT 120
 DB 61 MVAIAIYVKKKORTKTDVYTLINAVADLLFTLPWANAANAVGWLGIKMKCTITALT 120
 QY 121 LNFVSGMOFLACISIDRYAVAVTKVPQSQGVGKPCWIFCFVMAAAILISIPOLVFTYND 180
 DB 121 LNFVSGMOFLACISIDRYAVAVTKVPQSQGVGKPCWIFCFVMAAAILISIPOLVFTYND 180
 QY 121 LNFVSGMOFLACISIDRYAVAVTKVPQSQGVGKPCWIFCFVMAAAILISIPOLVFTYND 180
 DB 121 LNFVSGMOFLACISIDRYAVAVTKVPQSQGVGKPCWIFCFVMAAAILISIPOLVFTYND 180
 QY 181 NARCIPIPRYLGTSKALIIOMLEICIGFVVPFLINGVCYFRTARTLMKPNIKISRPLK 240
 DB 181 NARCIPIPRYLGTSKALIIOMLEICIGFVVPFLINGVCYFRTARTLMKPNIKISRPLK 240
 QY 241 VLLTVIVIVITVQLPNIYKFCRAIDIIYSLITSCMSKRMDAIOTVESIALFHSCLNP 300
 DB 241 VLLTVIVIVITVQLPNIYKFCRAIDIIYSLITSCMSKRMDAIOTVESIALFHSCLNP 300
 QY 301 ILYVFGASFKYVVMVAKKYGSMROROSVEEFPDSEPTPTSTFST 350
 DB 301 ILYVFGASFKYVVMVAKKYGSMROROSVEEFPDSEPTPTSTFST 350

RESULT 2

CKRB_BOVIN ID CKRB_BOVIN STANDARD; PRT; 350 AA.
 AC P35350;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE C-C chemokine receptor type 11 (C-C-CKR-11) (CCR-11)
 GN Name=CCRL1; Synonyms=CCR11;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 NC NCB1_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tongue;
 RX MEDLINE=93326166; PubMed=8392843;
 RA Matsuo K., Mori T., Aoki U., Sato T., Kurihara K.;
 RT "Identification of novel members of G-protein coupled receptor
 RT superfamily expressed in bovine taste tissue."
 RL Biochem. Biophys. Res. Commun. 194:504-511(1993).
 CC -1- FUNCTION: Receptor for SCYA2/MCP1, SCYA8/MCP2, SCYA13/MCP4,
 CC SCYA19/MIP3B/ELC, SCYA21/SLC and SCYA25/TECK (by similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in circumvallate and fungiform
 CC papillae, olfactory epithelium and lung. Lower expression in
 CC liver, kidney and tongue epithelium bearing no taste papillae.
 CC Very low expression in the cerebral cortex of the brain.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC or send an email to license@isb-sib.ch).

Query Match

89.1%; Score 1620; DB 1; Length 350;

Best Local Similarity 86.0%; Pred. No. 3,3e-91;
Matches 301; Conservative 27; Mismatches 22; Indels 0; Gaps 0;

QY 1 MLEONQSTDYEEENMGNTDYQSYELICIKEDYREBAKFLPYFLITVPIGLAGNS 60
DB 1 MAVEYNQSTDYEEENMGNTDYQSYELICIKEDYREBAKFLPYFLITVPIGLAGNS 60
QY 61 MVAIAYKKQRTKTDVYILNLAVALDLLFTLPPMAVNAVHGVGLGKIMCKITSAVLT 120
DB 61 TVAAIAYKKQRTKTDVYILNLAVALDLLFTLPPMAVNAVHGVGLGKIMCKITSAVLT 120
QY 121 LNFVSGMOFLACISIDRYAVAVTKVPSQSGVGCPCWIIICFCVMAAAILISPOLVFTVND 180
DB 121 VNFVSGMOFLACISIDRYAVAVTKVPSQSGVGCPCWIIICFCVMAAAILISPOLVFTVND 180
QY 181 NARCIPFPYVLTGSKKALIQMLEICIGFVVPFLNGVCYFIFARTLMKMPNIKISRPK 240
DB 181 KARCVPFPYVLTGSKKALIQMLEICIGFVVPFLNGVCYFIFARTLMKMPNIKISRPK 240
QY 241 VLTAVIVFIVTQLPVNIYFCRAIDITVSLTSCMSKRMDAIQOVETISIALPHSCINP 300
DB 241 VLTAVIVFIVTQLPVNIYFCRAIDITVSLTSCMSKRMDAIQOVETISIALPHSCINP 300
QY 301 ILVYFGASFCNVYMKVAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350
DB 301 VLVYFGTSFCNVYMKVAKKYGSMRQROSVSEFPDSEGPTEPTSTFSI 350

RESULT 3
092413 PRELIMINARY; PRT; 350 AA.
ID 092413
AC 092413
DT 01-DEC-2001 (TEMBLrel. 19, Created)
DT 01-DEC-2001 (TEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Chemokine receptor CCR11 (Mus musculus 3 days neonate thymus CDNA,
Riken full-length enriched library, clone:A630091E18 product:CHEMOKINE
RECEPTOR CCR11 homolog).
DE Name=CCR11;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20519697; PubMed=11063828; DOI=10.1016/S0165-5728(00)00371-4;
RA Dorf M.B., Berman M.A., Tanabe S., Heesen M., Luo Y.;
RT "Astrocytes express functional chemokine receptors.";
RL J. Neuroimmunol. 111:109-121(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX MEDLINE=20519697; PubMed=11063828; DOI=10.1016/S0165-5728(00)00371-4;
RA Dorf M.B., Berman M.A., Tanabe S., Heesen M., Luo Y.;
RT "Astrocytes express functional chemokine receptors.";
RL J. Neuroimmunol. 111:109-121(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Riken PANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;

RA The PANTOM Consortium.
RA the Riken Genome Exploration Research Group Phase I & II Team;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=2049374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carninci P., Shibata Y., Hayatsu N., Suganara Y., Shibata K., Itoh M.,
RA Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subcloning of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [7]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RX MEDLINE=20510913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
RA Konno H., Akiyama J., Nishi K., Kitsuina T., Taahiro H., Itoh M.,
RA Sumi N., Iehi Y., Nakamura S., Harada M., Nishine T., Harada A.,
RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujisawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanishi M.,
RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "Riken integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [8]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Thymus;
RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,
RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura Y.,
RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
RA Saito R., Saitoh H., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Tagawa A., Takahashi F., Takaku-Akashira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL: AF306532; AAK81712.1; -
DR EMBL: AK042430; BAC31258.1; -
DR MGI: MGI:2181676; Ccr11.
DR GO: GO:0016021; C: integral to membrane; IEA.
DR GO: GO:0016493; F: C-C chemokine receptor activity; IEA.
DR GO: GO:0004872; F: receptor activity; IEA.
DR GO: GO:0001584; F: rhodopsin-like receptor activity; IEA.
DR GO: GO:0007186; P: G-protein coupled receptor protein signaln. . . IEA.
DR Pfam: PF00001; 7tm.1; 1.
DR PRINTS: PRO0657; CCHEMOKINER.
DR PRINTS: PRO1558; CHEMOKINER1.
DR PRINTS: PRO0237; GPCRHDOPSN.
DR DR PROSITE: PS00237; G_PROTEIN_RECP_F1_1; 1.
DR DR PROSITE: PS02622; G_PROTEIN_RECP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane;
SQ SEQUENCE 350 AA; 39530 MW; C5PFD9DC949CECCF CRC64;

Query Match 87.7%; Score 1596; DB 2; Length 350;
Best Local Similarity 85.4%; Pred. No. 9.4e-90;
Matches 299; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

QY 1 MLEONQSTDYEEENMGNTDYQSYELICIKEDYREBAKFLPYFLITVPIGLAGNS 60
DB 1 MAVEYNQSTDYEEENMGNTDYQSYELICIKEDYREBAKFLPYFLITVPIGLAGNS 60
QY 61 MVAIAYKKQRTKTDVYILNLAVALDLLFTLPPMAVNAVHGVGLGKIMCKITSAVLT 120
DB 61 TVAAIAYKKQRTKTDVYILNLAVALDLLFTLPPMAVNAVHGVGLGKIMCKITSAVLT 120

AC 08QZM9;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Chemokine receptor CCR1.
 DE Name=CCR1;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10930;
 RN 11)
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Svj.
 RA Thomson J.R., Nibbs R.J.
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL; AY072796; AAL68400.1; -
 DR EMBL; AY072938; AAL68962.1; -
 DR MGD; MGI:2181676; Ccr1l.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO; GO:0007186; P:G-protein coupled receptor protein signaling. . .; IEA.
 DR InterPro: IPR005383; CC_11_receptor.
 DR InterPro: IPR000355; Chk1n_receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam; PF00001; 7tm_1; 1.
 DR PRINTS; PR00657; CCHEMOKINER.
 DR PRINTS; PR01558; CHEMOKINER11.
 DR PRINTS; PR00237; GPCRHOPOSPN.
 DR PROSITE; PS00237; G_PROTEIN_RECPT_P1_1; 1.
 DR PROSITE; PS0262; G_PROTEIN_RECPT_P1_2; 1.
 DR G-protein coupled receptor; Receptor; Receptor; Transmembrane.
 SQ SEQUENCE 350 AA; 39544 MW; D017CC29749CECD5 CRC64;

Query Match 87.6%; Score 1593; DB 2; Length 350;
 Best Local Similarity 85.1%; Pred. No. 1,4e-89;
 Matches 298; Conservative 27; Mismatches 25; Indels 0; Gaps 0;

QY 1 MALEQNSTDYEEENMGTYDSQYELICIKEDVREFAKVLPVFLTIIVFIGLAGNS 60
 DB 1 MALEINQSAEYEEENMGTYDSQYELICIKEDVREFAKVLPVFLTIIVFIGLAGNS 60
 QY 61 MVVAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAVHGVLGKIMKITSALYT 120
 DB 61 VVVAIYAYKKORTKTDVYILNLAVADLLFLTPFWAVNAVHGVLGKIMKITSALYT 120
 QY 121 LNPVSGMOPLACISIDRYVAVTVPSSQGVGKPCWIIICPVMMAAIILSLPOLVFTTND 180
 DB 121 VNPVSGMOPLACISIDRYVAVTVPSSQGVGKPCWIIICPVMMAAIILSLPOLVFTTND 180
 QY 181 NARCTPIPRVYLGTSKALIQMLEICIGFVVPFLINGVCYFTARTLMKPNIKISRLPK 240
 DB 181 NARCTPIPRVYLGTSKALIQMLEICIGFVVPFLINGVCYFTARTLMKPNIKISRLPK 240
 QY 241 VLLTVIVETVQLPYNIVKPCRAIDIIYSLITSCNMSKRMIDIAIQTESIALFHSCLNP 300
 DB 241 VLLTVIVETVQLPYNIVKPCRAIDIIYSLITSCNMSKRMIDIAIQTESIALFHSCLNP 300
 QY 301 ILYVFGASFKYVMVAKKYGSROROSVEFPDSDGPTPTSTPSI 350
 DB 301 ILYVFGASFKYVMVAKKYGSROROSVEFPDSDGPTPTSTPSI 350

RESULT 6
 063ZL5 PRELIMINARY; PRT; 356 AA.
 AC 063ZL5;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)

DE Hypothetical protein.
 OS Xenopus laevis (African Clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI_TaxID=8355;
 RN 11)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Straube R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative".
 RL Dev. Dyn. 225:384-391(2002).
 RN 12)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straube R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.B.,
 RA Brownstein M.J., Usdin T.B., Tothlyuk S., Carninci P., Prange C.,
 RA Rana S.S., Loguella N.A., Peters G.D., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Pahey J., Helton E., Ketterman M., Madan A.C., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Kravitz M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN 13)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Whole;
 RX Klein S., Gerhard D.S.;
 RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC082897; AAH82897.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 356 AA; 40514 MW; 2B4FAEA6561487A CRC64;

Query Match 58.8%; Score 1070; DB 2; Length 356;
 Best Local Similarity 60.8%; Pred. No. 1e-57; 81; Indels 6; Gaps 3;
 Matches 211; Conservative 49; Mismatches 81; Indels 6; Gaps 3;

QY 8 STDYEEENMGTYDSQYELICIKEDVREFAKVLPVFLTIIVFIGLAGNSMVAIYA 67
 DB 12 TENDVEYDGT--TPYGNVYBELCEKEVRFQFIPLPFAVAVFIGVAGNSLVVAIYS 69
 QY 68 YKKORTKTDVYILNLAVADLLFLTPFWAVNAVHGVLGKIMKITSALYTINFSGV 127
 DB 70 YKKMKSCTDVYILNLAVADLLFLTPFWAVNAVHGVLGKIMKITSALYTINFSGV 129
 QY 128 OFLACISIDRYVAVTVPSSQGVGKPCWIIICPVMMAAIILSLPOLVFTV--NNARC 184
 DB 130 OFLACISIDRYVAVTVPSSQGVGKPCWIIICPVMMAAIILSLPOLVFTV--NNARC 189
 QY 185 IPFPRVYLGTSKALIQMLEICIGFVVPFLINGVCYFTARTLMKPNIKISRLPKVLT 244
 DB 190 LPVYPRDYKQQTVAIQILBIKFCFLPFLVWVFCVSAAKIVLTKPNIKRSRLKVLTA 249
 QY 245 VVIVFIVTOLPYNIVKPCRAIDIIYSLITSCNMSKRMIDIAIQTESIALFHSCLNP 304
 DB 250 VVGVPFLVTLPLYNIVKPCRAIDIIYSLITSCNMSKRMIDIAIQTESIALFHSCLNP 309
 QY 305 FNGASFKYVMVAKKYGSROROSVEFPDSDGPTPTSTPSI 350

DB 310 FMGTFKCYISKIARCCSGSLRQRJHSTREFSMHSENVHETSSFSI 356

RESULT 7

Q9ESK1 PRELIMINARY; PRT; 221 AA.
AC Q9ESK1;
DT 01-MAR-2001 (TREMBLrel. 16, Last created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Putative G-protein coupled receptor GPCR14 (Fragment).
GN Name=Gpcr14;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Harian Sprague-Dawley;
RA Carroll S.L., Miller M.L., Benedict-Hamilton H.M.;
RL Submitted (Sep-1998) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF090348; AAG24470.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR005382; CC 10 receptor.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR01557; CHEMOKINER10.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
FT G-protein coupled receptor; Receptor; Transmembrane.
FT NON_TER 1 1
FT NON_TER 221 221
SQ SEQUENCE 221 AA; 24342 MW; 5622DD6073738A6C CRC64;

Query Match 50.1%; Score 912; DB 2; Length 221;
Best Local Similarity 83.3%; Pred. No. 3e-48;
Matches 169; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 96 FFAVNAVHGWATGKINCKITTSALYTLNFSGMOFLACISIDRVAVATKPSQSGVGKPCW 155
DB 19 FFAVNAVHGMIIIGKMKCKVTSALYTNFVSGMOFLACISIDRVAVATKPSQSGVGKPCW 78
QY 156 IICFCVMAAILLSIPOLVFYVNDNARCIPIPRVYLGTSMKALIQMLEICIGFVVPFLI 215
DB 79 IICCCWTAALISTIQOLVFYVNDNARCIPIPRVYLGTSMKALIQMLEICIGFVVPFLI 138
QY 216 MGVCFEITARTLMKMNINIKISRLKVLTVVIVITQLPYNIYKFCRAIDIIYSLTISC 275
DB 139 MGVCFAMTARKLIKMNINIKSRRLRVLLAVVVFYTRLPYNNVKKCGAIDAIYLLITNC 198
QY 276 NMSKMDIAIQTESIALFHSCL 298
DB 199 DMSKMDVAIQTESIALFHSCL 221

RESULT 8

Q6YT47 PRELIMINARY; PRT; 369 AA.
AC Q6YT47;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Chemokine (C-C motif) receptor 9 isoform A (Chemokine C-C motif receptor 9).
GN Name=CCR9;

OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxId=98823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (Jan-2003) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Shinkai H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (Sep-2003) to the EMBL/Genbank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (by similarity).
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AP06184; BAD08643.1; -
DR EMBL; AB119263; BAD12126.1; -
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
DR InterPro; IPR004069; CC 9 receptor.
DR InterPro; IPR000355; Chemokine_receptor.
DR InterPro; IPR00276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm.1; 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01531; CHEMOKINER9.
DR PRINTS; PR00237; GPCR_RHODPSN.
DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 369 AA; 41967 MW; DEBF76538600620 CRC64;

Query Match 36.4%; Score 663; DB 2; Length 369;
Best Local Similarity 38.4%; Pred. No. 6.5e-33;
Matches 129; Conservative 68; Mismatches 117; Indels 22; Gaps 5;

QY 2 ALEQNSTDYEEENMGTYDYDQY---ELICIKEDVREFAKVPLPVLITVYVIGLAG 58
DB 8 SLMPNMPDYGXDARP--SIEDYGNFTFDLCKKNHVGQFASHPLPPLVYLVIGANG 65
QY 59 NSMVVAIYVYKKQRTDVIYLNLAVDLLFLTPFAVNAVHGWATGKINCKITTSAL 118
DB 66 NSLVILVWYCTRVKTMDFLNLADLTLVLPFAVNAVHGWATGKINCKITTSAL 125
QY 119 YTLNFPVSGMOFLACISIDRVAVATKPSQSGVGKPCW-----IICFCVMAAILLS 169
DB 126 YKMFYSCVLLTMCISVDRIYIAQ----AVRAQTRQKRLLYSKVCFYVWVMAALC 180
QY 170 IFOLVFYV---NDNARCIPIPRVYLGTSMKALIQMLEICIGFVVPFLIMGVCFITART 226
DB 181 IPELILSYQKEHDAICMNYVPSDESTNLKSAVLKYLIGFLPFFVMAACCTYIIHT 240
QY 227 LMKMPNIKISRLKVLTVVIVITQLPYNIYKFCRAIDIIYSLTSCMSGRMDIAIQ 286
DB 241 LIOAKKSSGKALKKVTITVLFVFLVLSQFPYNCVLLQOTIDAYTMFSSCAVSTNDICRQ 300
QY 287 VTESIALFHSCLNPIIYVFMGASPKYVWKVAKKYG 322
DB 301 VTQTLAFHSHCLNPIIYVFMGASPKYVWKVAKKYG 336

RESULT 9

CKR7_HUMAN STANDARD; PRT; 378 AA.
AC P32248;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE C-C chemokine receptor type 7 precursor (C-C CKR-7) (CCR-7) (MIP-3 beta receptor) (BBV-induced G protein-coupled receptor 1) (BB1) (BLR2).
GN Name=CCR7;

GN Name=CCR7; Synonym=CMKBR7, EB1, EV11;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 (1)
 RP SEQUENCE FROM N.A.
 RP MEDLINE=9318173; PubMed=8383238;
 RA Birkenbach M.P., Josefsen K., Valamanchi R.R., Lenoir G.M.,
 Kieff E.;
 "Epstein-Barr virus-induced genes: first lymphocyte-specific G
 protein-coupled peptide receptors.";
 RT J. Virol. 67:2209-2220(1993).
 [2]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Placenta;
 RC MEDLINE=95154835; PubMed=7851893;
 RA Schweickart V.L., Raport C.J., Godliska R., Byers M.G., Eddy R.L. Jr.,
 Shows T.B., Gray P.W.;
 "Cloning of human and mouse EB1, a lymphoid-specific G-protein-
 coupled receptor encoded on human chromosome 17q12-q21.2.";
 RT Genomics 23:643-650(1994).
 [3]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 Brownstein M.J., Ueda T.B., Tohyuki S., Carninci P., Prange C.,
 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 Bosa S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 Butcherfield V.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
 Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Receptor for the MIP-3-beta chemokine. Probable mediator
 of EBV effects on B lymphocytes or of normal lymphocyte functions.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- TISSUE SPECIFICITY: Expressed in various lymphoid tissues and
 activated B and T lymphocytes, strongly up-regulated in B cells
 infected with Epstein-Barr virus and T cells infected with
 herpesvirus 6 or 7.
 CC -1- INDUCTION: By EBV.
 CC -1- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.1sb-sib.ch/announce/>
 or send an email to license@1sb-sib.ch).
 CC -----
 CC EMBL, L08176; AAA58615.1; -
 DR EMBL, L31584; AAA74230.1; -
 DR EMBL, L31583; AAA74230.1; JOINED.
 DR EMBL, L31581; AAA74231.1; -
 DR EMBL, BC035343; AAA35343.1; -
 DR PIR, A45680; A45680.
 DR PIR, B55735; B55735.
 DR HSPF, P34996; 1DDO.

DR Genew: HGNC:1608; CCR7.
 DR MIM: 600242; -
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0004950; F: chemokine receptor activity; TAS.
 DR GO: GO:0004930; F: G-protein coupled receptor activity; TAS.
 DR GO: GO:0019735; P: antimicrobial humoral response (sensu Verte. . .); TAS.
 DR GO: GO:0006935; P: chemotaxis; TAS.
 DR GO: GO:0007204; P: cytosolic calcium ion concentration elevation; TAS.
 DR GO: GO:0006954; P: inflammatory response; TAS.
 DR InterPro: IPR001718; CC_7_receptor.
 DR InterPro: IPR000355; Chkline_receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsn.
 DR Pfam: PF00001; 7tm.1; 1.
 DR PRINTS: PR00237; GPCRHOPOPSN.
 DR PROSITE: PS00237; G_PROTEIN_RECPT_F1_1; 1.
 DR PROSITE: PS0262; G_PROTEIN_RECPT_F1_2; 1.
 KW G-protein coupled receptor; Glycoprotein; Signal; Transmembrane.
 FT SIGNAL 1 24
 FT CHAIN 25 378
 FT DOMAIN 25 59
 FT TRANSMEM 60 86
 FT DOMAIN 87 95
 FT TRANSMEM 96 116
 FT DOMAIN 117 130
 FT TRANSMEM 131 152
 FT DOMAIN 153 170
 FT TRANSMEM 171 191
 FT DOMAIN 192 219
 FT TRANSMEM 220 247
 FT DOMAIN 248 263
 FT TRANSMEM 264 289
 FT DOMAIN 290 313
 FT TRANSMEM 314 331
 FT DOMAIN 332 378
 FT CARBOHYD 36 36
 FT DISULFID 129 210
 FT CONFLICT 182 183
 FT CONFLICT 337 337
 SQ SEQUENCE 378 AA; 42874 MM; D4CB4213841A1BD4 CRC64;
 Query Match 36.2%; Score 659; DB 1; Length 378;
 Best Local Similarity 38.7%; Pred. No. 1, 2e-32;
 Matches 144; Conservative 66; Mismatches 124; Indels 38; Gaps 7;
 1 MAFQNSQDYEEENENGTDYSELCIKEDVREKAVFLPFLTVPIYGLAGNS 60
 21 VCLCODEVDDYIGDNT--TVDTLFEISLCSKQDVRNFKAMFLPTMYSICFVGLGNG 77
 61 MVAIYAYKKORTKTDVYILNLAVDLLFLPFWANAVHGVIGKIMCKITSALYT 120
 78 LVVLYTYFRRLKTMIDTYILNLAVDILFLTLTPMAWSAKSWFGVHFCILTAIYK 137
 121 LNFVSGQPLACISIDRYAVAVTKVPS---QSGVGRPCWIIQPCVMAAIIISIPOLVFY 176
 138 MSFSPGMLLLICSIDRYAVAIQAVSAHHRBARVLLISLSCGVIIATVLSIPELVS 197
 177 TVNDNA-----RCIPFPYVLTGSMKALIQMLEICGFVVPFLIMVCFTIRTKMKP 231
 198 DLRSSSEQAMCSLTIEH---VEAFITIQVQMGVFLPFLAMSFCLVIRTLQAR 254
 232 NIKISRLVLLVTVVFLVTOLPVNIYVFCRAIDIIYSLSCNNSKMDIAIOVTEI 291
 255 NERNRAIKVILVAVVFLVFPQPNGVLAQIVANFNITSSICELSKQNLIAVDYISL 314
 292 ALFHSCLNPLLYVFMGASFKVYMKVAKYGV-----SW-----RROROSVEEPPD 337
 315 ACVRCVNPFLVAFIVKFRNDLPKFLKDLGCLSGQGLQWWSGCRHRRSSMSVE----- 369
 338 SEGGTEPTSTFS 349
 370 ---AETTTTFS 377

RESULT 10

06YT46 PRELIMINARY; PRT; 357 AA.
AC 06YT46;
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DE Chemokine (C-C motif) receptor 9 isoform B.
GN Name=CCR9;
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Shikata H., Morozumi T., Toki D., Muneta Y., Awata T., Uenishi H.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AB006184; BAD08644.1; -.
DR GO; GO:0016021; C:intracellular to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:G-protein-coupled receptor activity; IEA.
DR GO; GO:0007186; P:G-protein-coupled receptor protein signaling. . .; IEA.
DR InterPro; IPR004069; CC 9 receptor.
DR InterPro; IPR000355; Chkline_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1, 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR01531; CHEMOKINER9.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_P1_2; 1.
KM G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 357 AA; 40725 MW; 93F80F90F91337A CRC64;

Query Match 36.1%; Score 657; DB 2; Length 357;

Best Local Similarity 38.7%; Pred. No. 1.5e-32;
Matches 127; Conservative 67; Mismatches 112; Indels 22; Gaps 5;

QY 10 DYVEENENMGTYDYQY--ELICTEDREFAKVPFLVFLTVFVIGLAGNSMVAIY 66
DB 4 DYGYDADTP--SIDEDYFTFDLFCCKNHRCPASHFLPLVYLVEIVGAVNSLVILVY 61
QY 67 AYYKQRTDTPDYVYLNLAVADLLFLTPMAVNAHGWLGKIMCKITSAULTNLFPVGS 126
DB 62 WCTRYKRTMDLFLNLALADLLFLTPMAVNAHGWLGKIMCKITSAULTNLFPVGS 121
QY 127 MOFLACISIDRYAVAVTVPSQSGVGRPCW-----IICFCVMAAILLSIPQLVFY 177
DB 122 VLLIMCISDRIYALNQ-----AMRAQITWRQKRLYSKLVCFVWMAALCIPELLVSG 176
QY 178 V--NDNARCIPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIK 234
DB 177 VKEHHAICTWYYPDESGTNLSAVLTKVILGFELPFWMACCYTIIHTLIQAKSS 236
QY 235 ISRLPLVLLTVVVFVITQLPYNIYKFCRAIDIIYSLITSCKNSKMDIAIQTSTALF 294
DB 237 KHAALKVITVLLVFLVPSOPFNVCVLLVQITIDAYTMFISCAVSTINDICFQVLTITAF 296
QY 295 HSCINPLLYFMGASFKNYMKVAKKYG 322
DB 297 HSCINPLVLYFVGERFRRLVLTNLKLG 324

RESULT 11

08HZR6 PRELIMINARY; PRT; 378 AA.
AC 08HZR6;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)

DE CC chemokine receptor 7.
GN Name=CCR7;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22471764; PubMed=12406887; DOI=10.1182/Blood-2002-08-2653;
RT Choi Y.K., Fallert B.A., Murphy-Corb M.A., Reinhardt T.A.;
RT "Simian immunodeficiency virus dramatically alters expression of
RT homeostatic chemokines and dendritic cell markers during infection in
RT vivo."

CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR EMBL; AF508731; AA047099.2; -.
DR GO; GO:0016021; C:intracellular to membrane; IEA.
DR GO; GO:0016493; F:C-C chemokine receptor activity; IEA.
DR GO; GO:0004872; F:receptor activity; IEA.
DR GO; GO:0001584; P:G-protein-coupled receptor activity; IEA.
DR GO; GO:0007186; P:G-protein-coupled receptor protein signaling. . .; IEA.
DR InterPro; IPR001718; CC_7_receptor.
DR InterPro; IPR000355; Chkline_receptor.
DR InterPro; IPR000276; GPCR_Rhodpsn.
DR Pfam; PF00001; 7tm_1, 1.
DR PRINTS; PR00657; CCHEMOKINER.
DR PRINTS; PR00237; GPCR_RHODOPSIN.
DR PROSITE; PS00237; G_PROTEIN_REC_P1_1; 1.
DR PROSITE; PS00262; G_PROTEIN_REC_P1_2; 1.
KM G-protein coupled receptor; Receptor; Transmembrane.
SQ SEQUENCE 378 AA; 42876 MW; D031B848B29F08EF CRC64;

Query Match 36.1%; Score 657; DB 2; Length 378;

Best Local Similarity 38.9%; Pred. No. 1.5e-32;
Matches 143; Conservative 65; Mismatches 122; Indels 38; Gaps 7;

QY 5 ONOSTDYVEENENMGTYDYQYELICTEDREFAKVPFLVFLTVFVIGLAGNSMVA 64
DB 25 QDEVDYDYGDMT--TVDTYTFESLCSKDVANFAMFLPIMYSILICVGLGKGLVVL 81
QY 65 IYAYKQRTDTPDYVYLNLAVADLLFLTPMAVNAHGWLGKIMCKITSAULTNLFV 124
DB 82 TVIYFRLTMDTLYLNLAVADLLFLTPMAVNAHGWLGKIMCKITSAULTNLFV 141
QY 125 SGMOFLACISIDRYAVAVTVPS---QSGVGRPCWITICVMAAILLSIPQLVFYTVND 180
DB 142 SGMLLACISIDRYAVAVTVPS---QSGVGRPCWITICVMAAILLSIPQLVFYTVND 201
QY 181 NA-----RCIPPIPRYLGTSMKALIQMLEICIGFVVPFLIMGVCFITARTLMKPNIK 235
DB 202 SSSEOMRSCSLTTH--VEAFITIOVAGVIGFVPLAMSFYVITRTILOANRPER 258
QY 236 SHPLKVLTVVVFVITQLPYNIYKFCRAIDIIYSLITSCKNSKMDIAIQTSTALF 295
DB 259 NKAIKVITVLLVFLVPSOPFNVCVLLVQITIDAYTMFISCAVSTINDICFQVLTITAF 318
QY 296 SCINPLLYFMGASFKNYMKVAKKYG-----SW-----RRRQSVVEFPFSPSE 341
DB 319 CCVNPFLVAFIGVFRNDLFLKFDGLCSLOBOLROMSSCRHRRSSMSVE----- 369
QY 342 TEPTSTES 349
DB 370 AETTTES 377

RESULT 12

CKR7 MOUSE
ID CKR7_MOUSE STANDARD; PRT; 378 AA.
AC P47774;
DT 01-FEB-1996 (Rel. 33, Created)

QY 5 QNOSTYIYYEENMGTYDYSQVELICTEDVREPAKFLPVLFTIVFVIGLAGNSMYVA 64

Db	25	QDEVTDDYIGENT--TVDVTLYESVCFKQVRNFKAMFLPLMYSVICFVGLANGVIL	8
Qy	65	IVAYYKQKRTKDVYILNLAADVLLFLPLPMANAVHGVLLKINCKITSALTYNFV	12
Db	82	TYIYFKRLTKMDVYILNLAADVLLFLPLPMAYSEAKSWIFGVYLCGFGIYKLSFF	14
Qy	125	SGNQPLACISIDRYAVAVTKVPSQSG-----VGKPCMIICECVMAALLISIQVLEYT	17
Db	142	SGMLLLCTISIDRYAVAVTKVPSQSG-----LSCVGIWMLALFLISTEELVYSG	19
Qy	178	VNDNA-----RCIPFPRYIAGTSMKAL--IQMLEICIGFVVPFLIMGVETARTILMKM	23
Db	199	LQNGSDEBTLRC-----SLVSAQVBAITLIOAQGVFVLVPLMLAMSCVILIIRTLIQA	25
Qy	231	PNIKISPLKVLTVIVYVITVITQLPYNYIKFCRAIDIIYSILTSCNSKMDIAYTES	29
Db	254	RNERKKAIKVILIAVAVVVFVITQLPYNGVILAQTVANFNITNSSCETSQKQINIVDYTS	31
Qy	291	IALFHSCLNPIIYVFMGASFKKYVWKVAKKXGSMRQR-----QSVTEEPFDSQPT	34
Db	314	LAIVRCVAVPFIYAFIAGVFKRSDFLKLPRDGJGUSQERLHMWSSCRHVRNASSVME--AE	37
Qy	344	PTSTFS 349	
Db	372	TTTTFS 377	
RESULT 13			
OGP68:			
ID	OGP68	PRELIMINARY:	PRT: 358 AA.
AC	OGP68		
DT	05-JUL-2004 (TEMBLrel. 27, Created)		
DT	05-JUL-2004 (TEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004 (TEMBLrel. 27, Last annotation update)		
DE	MGC80638 protein.		
GN	Name=MGC80638:		
OS	Xenopus laevis (African clawed frog).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;		
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;		
OC	Xenopodidae; Xenopus.		
OX	NCBI_TaxID=8355;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSE=Spleen;		
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;		
RA	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,		
RA	Klausner R.D., Collins F.S., Wagner K.H., Scheffer C.F., Bhat N.K.,		
RA	Altschul S.F., Zeeberg B., Buetow K.H., Moore T., Wax S.I., Hsieh F.,		
RA	Hopkins R.F., Jordan H., Moore T., Wang J., Hsieh F.,		
RA	Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,		
RA	Sapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,		
RA	Brownstein M.J., Ushin T.B., Toshiyuki S., Carninci P., Prange C.,		
RA	Raha S., Liguellano N.A., Peters G.J., Abrahamson R.D., Mullaby S.J.,		
RA	Boak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,		
RA	Richardson S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,		
RA	Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,		
RA	Fahney J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,		
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,		
RA	Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,		
RA	Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,		
RA	Krzywicki M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,		
RA	Jones S.J., Marra M.A.;		
RT	"Generation and initial analysis of more than 15,000 full-length human		
RT	and mouse cDNA sequences.";		
RL	Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	TISSE=Spleen;		
RX	MEDLINE=22311132; PubMed=12454917; DOI=10.1002/dvdy.10174;		
RA	Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,		
RA	Richardson P.,		
RT	"Genetic and genomic tools for Xenopus research: The NIH Xenopus		
RT	initiative.";		

RL Dev. Dyn. 225:384-391 (2002).
 (3)
 RN SEQUENCE FROM N.A.
 RP TISSUE=Splice.
 RC Klein S., Gerhard D.S.;
 RA Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RL SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL: BC073273; AH73273.1; -.
 DR GO: GO:0016021; C:integral to membrane; IEA.
 DR GO: GO:0016493; F:C-C chemokine receptor activity; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0001584; F:rhodopsin-like receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor protein signalin. . .; IEA.
 DR InterPro: IPR001718; CC 7 receptor.
 DR InterPro: IPR000355; Chklike receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsin.
 DR Pfam: PF00001; 7tm_1, 1.
 DR PRINTS: PR00657; CCHEMOKINER.
 DR PRINTS: PR00641; CHEMOKINER7.
 DR PRINTS: PR00237; GPCR_RHODOPSIN.
 DR PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE: PS02652; G-PROTEIN RECP_F1_2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 KW SEQUENCE 358 AA; 40555 MW; DIF37C148823CAD5 CRC64;
 SQ

Query Match 35.7%; Score 649; DB 2; Length 358;
 Best local similarity 38.8%; Pred. No. 4.5e-32;
 Matches 144; Conservative 59; Mismatches 120; Indels 48; Gaps 10;

QY 4 EONQSTDYEEENENMGTYDYSQYELCIKEDVREFAKVFLPVFLITVFVIGLAGNSMVV 63
 DB EDVNSTD---ENVPYSTMDYSDLTQVCQKGDVTRFRSSFLPAMYITLICVLAGNGLVW 65
 QY 64 AIYAYKKQRTQDYVITLNAVDLLLPFPMVAVNAHGWTLGKIMCITATLTLP 123
 DB IRLYFNRLKNGDGYMLNLADIVFLTLTPMAVSVAKMWFGEEMCKITVCLKKMS 125
 QY 124 VSGMGQCLACISIDRYAVATKVPSSQ-----SGWGKPCWIIICFVMAAILLSI 170
 DB FSGMFLMCVSMERYAIYQAPSAHNRKTVISKLSSIG-----IWFALLLSI 176
 QY 171 POLVFYTVDNA---RCIPFPFYLTGTSKMLIQMLEICIGFVVPFLMGVCYFITARTL 227
 DB PELLYSGVNNNGVNMCI-IFSNSI-QSLSAKLIKISQMFPGFPLPIIMALCYCMIIRKL 234
 QY 228 MKMPNKKISBPLKVLTVIVFIVTQLPYIVFCALDIITISLISCSNMKMDALAIQY 287
 DB LQARNEEKKAIKVIITAIYVFAFQLPYNSVWLIRTFD---NGTDCSAKSLDIADVDV 290
 QY 288 TESIALFHSCLNPILVFMGASPKNYVMKVAKKYQ-----SWPROROSVE-EFPFDS 338
 DB TYSLAFPRCLNPLVIAIIGIKFRNDCLKFKDICTLSQKRTIEMSAKSRRTSPAMD 349
 QY 339 EGPTPEPTSTFS 349
 DB 350 ---TETTTFS 357

RESULT 14
 Q8CAGS2 PRELIMINARY; PRT; 378 AA.
 AC Q8CAGS2;
 DT 01-MAR-2003 (TEMBLrel. 23, Created)
 DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Mus musculus 16 days neonate thymus cDNA, RIKEN full-length enriched library, clone A130067M15 product:chemokine (C-C) receptor 7, full insert sequence.
 GN Name=Ccr7;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxId=10090;
 (1)
 RN SEQUENCE FROM N.A.
 RP STRAIN=C57BL/6J; TISSUE=Thymus;
 RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
 RA Carninci P., Hayashizaki Y.;
 RT "High-efficiency full-length cDNA cloning";
 RL Meth. Enzymol. 303:19-44 (1999).
 RN (2)
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
 RA RIKEN FANTOM Consortium;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690 (2001).
 RN (3)
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RA The FANTOM Consortium;
 RA the RIKEN genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs";
 RL Nature 420:563-573 (2002).
 RN (4)
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20499374; PubMed=11042159; DOI=10.1101/9r.145100;
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,
 RT "Normalization and subcloning of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes";
 RL Genome Res. 10:1617-1630 (2000).
 RN (5)
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RX MEDLINE=20530913; PubMed=11076861; DOI=10.1101/9r.152600;
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,
 RA Kono H., Akiyama J., Nishi K., Katsunai T., Tashiro H., Itoh M.,
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
 RA Fujitake S., Inoue K., Togawa Y., Izawa M., Ohara E., Watabiki M.,
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer";
 RL Genome Res. 10:1757-1771 (2000).
 RN (6)
 RN SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Thymus;
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoaka T., Hirozane T.,
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
 RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 DR EMBL: AK037965; BAC29909.1; -.
 DR MGD: MGI:103011; Ccr7.
 DR GO: GO:0005615; C:extracellular space; TAS.
 DR GO: GO:0016021; C:integral to membrane; TAS.
 DR GO: GO:0016493; F:C-C chemokine receptor activity; IMP.
 DR GO: GO:0006935; P:chemotaxis; IMP.
 DR GO: GO:0006955; P:immune response; IMP.
 DR InterPro: IPR001718; CC 7 receptor.
 DR InterPro: IPR000355; Chklike receptor.
 DR InterPro: IPR000276; GPCR_Rhodopsin.

DR Pfam: PF00001; Tm 1; 1.
 DR PRINTS: PR00657; CCHEMOKINER.
 DR PRINTS: PR00641; CHEMOKINER7.
 DR PRINTS: PR00237; GPCRKHODOPN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 KW SEQUENCE 378 AA; 42855 MW; F027451989B59683 CRC64;

Query Match 35.6%; Score 648; DB 2; Length 378;
 Best Local Similarity 38.6%; Pred. No. 5.5e-32;
 Matches 140; Conservative 67; Mismatches 128; Indels 28; Gaps 7;

QY 5 QNOSTDYEEENMGTYDYSQYELICIKEDYREPAKVFLLPVFLTVFVIGLAGNSMYYA 64
 DB 25 QDEVTDDYIGENT---TYDYTLYESVCFKDVNRKAMFLPLMYSVICFVGILGNGLVYL 81
 QY 65 IYAYYKQRTKTDVYILNLAVADLLFLTPMVAANAAGVGLGKIMCKITSAIYTLNFV 124
 DB 82 TYIYKRLKMTDYLNLAVADILFLMLPMAVSEAKSWIFGAYLCKSIGIYKLSFF 141
 QY 125 SGMQFLACISIDRYAAVTKVPS---QSGVGKPCWIIICPVMAAILLSIPOLVFYTVND 180
 DB 142 SGMILLICISIDRYAAVIAVQAVSAHRRARVLLISKLSICVIGIMLALFLSIPELYSGLQK 201
 QY 181 NA-----RCIPFPYRLGTSMAKAL--IQMLEICIGFVVPFLMGVCYFITAATMKMPNI 233
 DB 202 NSGEDTLRC-----SLVSAQVEALITTOVAQVGFVPLMLMSPCYLLIIRTLQARNF 256
 QY 234 KISRPLKVLTVIYIYITQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQVETSL 293
 DB 257 ENKAKIKVIAVAVVVFVQLPYNGVLAQTAVANFNITNSCETSQOLIAIADVTYSLAS 316
 QY 294 FHSCLNPLIYVFMGSAFKKYVKKVAKKYSWROR-----QSVKEPFDESGPTPTS 346
 DB 317 VRCVNPFLYAFITGVKFRSDLFKLFDLGLCLSGERLRHWSSCRHVNASVSM--AETTT 374
 QY 347 TFS 349
 DB 375 TFS 377

RESULT 15

ID Q6U2D6 PRELIMINARY; PRT; 378 AA.
 AC Q6U2D6
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
 DE Chemokine receptor 7-like protein.
 GN Name=Ccr7;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=BN; TISSUE=Lymph node;
 RA Quinlini G., Voland B., Hoffmeyer A.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
 CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
 DR EMBL: AY379972; AKR24573.1; -
 DR GO: GO:0016021; C:Integral to membrane; IEA.
 DR GO: GO:0016493; P:C-C chemokine receptor activity; IEA.
 DR GO: GO:0004872; F:receptor activity; IEA.
 DR GO: GO:0007186; P:G-protein coupled receptor activity; IEA.
 DR InterPro: IPR001718; CC_7_receptor.
 DR InterPro: IPR000355; ChmKine_receptor.
 DR InterPro: IPR000276; GPCR_Rhodopn.
 DR Pfam: PF00001; Tm 1; 1.
 DR PRINTS: PR00657; CCHEMOKINER.

DR PRINTS: PR00641; CHEMOKINER7.
 DR PRINTS: PR00237; GPCRKHODOPN.
 DR PROSITE: PS00237; G_PROTEIN_RECEP_F1_1; 1.
 DR PROSITE: PS00262; G_PROTEIN_RECEP_F1_2; 1.
 DR G-protein coupled receptor; Receptor; Transmembrane.
 KW SEQUENCE 378 AA; 42821 MW; A015E711DC4B521F CRC64;

Query Match 35.5%; Score 646; DB 2; Length 378;
 Best Local Similarity 38.0%; Pred. No. 7.2e-32;
 Matches 138; Conservative 68; Mismatches 129; Indels 28; Gaps 7;

QY 5 QNOSTDYEEENMGTYDYSQYELICIKEDYREPAKVFLLPVFLTVFVIGLAGNSMYYA 64
 DB 25 QDEVTDDYIGENT---TYDYTLYESVCFKDVNRKAMFLPLMYSVICFVGILGNGLVYL 81
 QY 65 IYAYYKQRTKTDVYILNLAVADLLFLTPMVAANAAGVGLGKIMCKITSAIYTLNFV 124
 DB 82 TYIYKRLKMTDYLNLAVADILFLMLPMAVSEAKSWIFGAYLCKSIGIYKLSFF 141
 QY 125 SGMQFLACISIDRYAAVTKVPS---QSGVGKPCWIIICPVMAAILLSIPOLVFYTVND 180
 DB 142 SGMILLICISIDRYAAVIAVQAVSAHRRARVLLISKLSICVIGITLAFLLSIPELYSGLQK 201
 QY 181 NA-----RCIPFPYRLGTSMAKAL--IQMLEICIGFVVPFLMGVCYFITAATMKMPNI 233
 DB 202 NSGEDTLRC-----SLVSAQVEALITTOVAQVGFVPLMLMSPCYLLIIRTLQARNF 256
 QY 234 KISRPLKVLTVIYIYITQLPYNIYKFCRAIDIIYSLITSCNMSKMDIAIQVETSL 293
 DB 257 ENKAKIKVIAVAVVVFVQLPYNGVLAQTAVANFNITNSCETSQOLIAIADVTYSLAS 316
 QY 294 FHSCLNPLIYVFMGSAFKKYVKKVAKKYSWROR-----QSVKEPFDESGPTPTS 346
 DB 317 VRCVNPFLYAFITGVKFRSDLFKLFDLGLCLSGERLRHWSSCRHVNASVSM--AETTT 374
 QY 347 TFS 349
 DB 375 TFS 377

Search completed: March 2, 2005, 04:23:08
 Job time : 72 secs

